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| **UTILITY PATENT APPLICATION TRANSMITTAL** *(Only for new nonprovisional applications under 37 CFR 1.53(b))* | Attorney Docket No. | 05686.0004.NPUS00/35-10(17108) | |
|---|---|---|---|
| | First Named Inventor or Application Identifier | | Karunanandaa |
| | Title | Nucleic Acid Molecules and Other Molecules Associated with Sterol Synthesis and Metabolism | |
| | Express Mail Label No. | | |

| **APPLICATION ELEMENTS** See MPEP chapter 600 concerning utility patent application contents | **ADDRESS TO:** | Assistant Commissioner for Patents Box Patent Application Washington, DC 20231 |
|---|---|---|

1. ☐ *Fee Transmittal Form (Form PTO-1082) *(Submit an original and a duplicate for fee processing)*

2. ☒ Specification [*Total Pages* 159 ] *(preferred arrangement set forth below)*
   - Descriptive title of the Invention
   - Cross References to Related Applications
   - Statement Regarding Fed sponsored R&D
   - Reference to Microfiche Appendix
   - Background of the Invention
   - Brief Summary of the Invention
   - Brief Description of the Drawings (if filed)
   - Detailed Description
   - Claims
   - Abstract of the Disclosure

3. ☐ Drawing(s) *(35 USC 113)* [*Total Sheets* ___ ]

4. Oath or Declaration [*Total Pages* ___ ]
   a. ☐ Newly executed (original or copy)
   b. ☐ Copy from a prior application (37 CFR 1.63(d)) *(for continuation/divisional with Box 17 completed)* *[Note Box 5 below]*
      i. ☐ DELETION OF INVENTOR(S) Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).

5. ☐ Incorporation By Reference *(useable if Box 4b is checked)* The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. ☐ Microfiche Computer Program *(Appendix)*

7. Nucleotide and/or Amino Acid Sequence Submission *(if applicable, all necessary)*
   a. ☒ Computer Readable Copy
   b. ☒ Paper Copy (identical to computer copy)
   c. ☒ Statement verifying identity of above copies

**ACCOMPANYING APPLICATION PARTS**

8. ☐ Assignment Papers (cover sheet & document(s))

9. ☐ 37 CFR 3.73(b) Statement *(when there is an assignee)* ☐ Power of Attorney

10. ☐ English Translation Document *(if applicable)*

11. ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations

12. ☐ Preliminary Amendment

13. ☒ Return Receipt Postcard (MPEP 503) (Two) *(should be specifically itemized)*

14. ☐ *Small Entity Statement(s) ☐ Statement filed in prior application, Status still proper and desired

15. ☐ Certified Copy of Priority Document(s) *(if foreign priority is claimed)*

16. ☐ Other:

*NOTE FOR ITEMS 1 & 14 IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C.F.R. § 1.27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F.R. § 1.28)

17. **If a CONTINUING APPLICATION**, *check appropriate box and supply the requisite information:*
   ☐ Continuation   ☐ Divisional   ☐ Continuation-in-part (CIP) of prior application No: /
   Prior Application Information: Examiner: ___ Group/Art Unit: ___

**18. CORRESPONDENCE ADDRESS**

☒ *Customer Number or Bar Code Label* 22930 *(Insert Customer No. or Attach bar code label here)*   or ☐ *Correspondence address below*

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| Signature | | Date | July 11, 2000 | | |

July 11, 2000

*Box Patent Applications*

Assistant Commissioner for Patents
Washington, D.C. 20231

Re:   U.S. Non-Provisional Utility Patent Application
Application No.: To Be Assigned
Filed:        Herewith
For:          **Nucleic Acid Molecules and Other Molecules**
              **Associated with Sterol Synthesis and Metabolism**
Inventors:   Balasulojini KARUNANANDAA *et al.*
Atty. Docket:  05686.0004.NPUS00/35-21(17108)

Sir:

The following documents are forwarded herewith for appropriate action by the U.S.
Patent and Trademark Office:

1.   Utility Patent Application Transmittal (PTO/SB/05);

2.   U.S. Utility Patent Application entitled:

**Nucleic Acid Molecules and Other Molecules Associated with**
**Sterol Synthesis and Metabolism**

and naming as inventors:

**Balasulojini KARUNANANDAA, Jaehyuk YU, and Ganesh M. KISHORE,**

the application consisting of:

a.   A specification containing:

(i)     __154__ pages of a description prior to the claims;

(ii)    ___3_ page of claims (_27_ claims);

(iii)   a one (1) page abstract; and

(iv)    __777__ pages of a sequence listing;

3.   A computer-readable diskette containing the sequence listing;

4.   Statement Regarding Sequence Submission; and

5.     Two (2) return postcards.
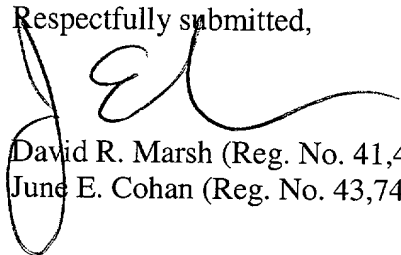
This application claims priority under 35 U.S.C §119(e) of U.S. Provisional Application No. 60/142,981, filed July 12, 1999.

This application is being filed without an executed Declaration, and without payment of official fees.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the sequence listing and the computer readable copy of the sequence listing submitted herewith in the above application are the same.

It is respectfully requested that, of the two attached postcards, one be stamped with the filing date of these documents and returned to our courier, and the other, prepaid postcard, be stamped with the filing date and unofficial application number and returned as soon as possible.

Respectfully submitted,

David R. Marsh (Reg. No. 41,408)
June E. Cohan (Reg. No. 43,741)

Enclosures

# IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Balasulojini KARUNANANDAA *et al.*

Appln. No.: To Be Assigned

Filed: July 11, 2000

For: Nucleic Acid Molecules and Other Molecules Associated with Sterol Synthesis and Metabolism

Art Unit: To Be Assigned

Examiner: To Be Assigned

Atty. Docket: 05686.0004.NPUS00/ 35-21(17108)
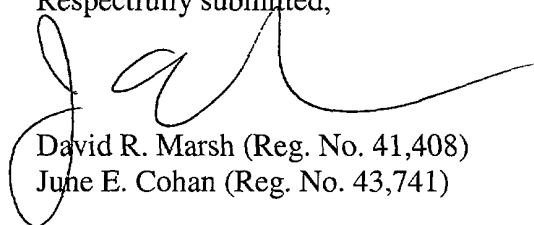
## Statement Regarding Sequence Submission

Assistant Commissioner for Patents
Washington, DC  20231

Sir:

  In accordance with 37 C.F.R. § 1.821(f), the paper copy of the Sequence Listing and the

computer readable copy of the Sequence Listing submitted herewith in the above-mentioned

application are the same.

Respectfully submitted,

David R. Marsh (Reg. No. 41,408)
June E. Cohan (Reg. No. 43,741)

Date:  July 11, 2000

Howrey Simon Arnold & White, LLP
Box 34
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# NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH STEROL SYNTHESIS AND METABOLISM

## FIELD OF THE INVENTION

This invention relates to the field of biotechnology, particularly as it pertains to the

5    production of sterols in a variety of host systems particularly plants. More specifically, the

invention relates to nucleic acid molecules encoding proteins and fragments of proteins

associated with sterol and phytosterol metabolism as well as the encoded proteins and fragments

of proteins and antibodies capable of binding to them. The invention also relates to methods of

using the nucleic acid molecules, fragments of the nucleic acid molecules, proteins, and

10    fragments of proteins. The invention also relates to cells, organisms, particularly plants, or seeds,

or progeny of plants, that have been manipulated to contain increased levels or overexpress at

least one sterol or phytosterol compound.

## BACKGROUND OF THE INVENTION

Sterols are a class of essential, natural compounds required by all eukaryotes to complete

15    their life cycle. The types of sterols produced and predominantly present within each of the

phylogenetic kingdoms varies. Plants produce a class of sterols called phytosterols. A

phytosterol called sitosterol predominates. In animals, cholesterol is typically the major sterol

while in fungi it is ergosterol.

Phytosterols from plants possess a wide spectrum of biological activities in animals and

20    humans. Phytosterols are considered efficacious cholesterol-lowering agents (Pelletier *et al.*,

*Annals Nutrit. Metab.* 39:291-295 (1995), the entirety of which is herein incorporated by

reference). Lower cholesterol levels are linked to a reduction in the risk to cardiovascular

disease. Phytosterols can also block cholesterol absorption in the intestine, which would also

lead to lower cholesterol levels. Thus, enhancing the levels of phytosterols in edible plants and

25    seeds, or products derived from these plants and seeds, may lead to food products with increased

nutritive or therapeutic value.

In one aspect, this invention provides these desirable plants and seeds as well as methods to produce them. Since, as will be discussed below, the genetic manipulation made possible by this invention involves families of related genes that cross phylogenetic boundaries, the effects are not limited to plants alone.

5 **Biochemistry of Sterol Synthesis**

A number of the important sterol biosynthetic enzymes, reactions, and intermediates have been described. Sterol synthesis uses acetyl CoA as the basic carbon building block. Multiple acetyl CoA molecules form the five-carbon isoprene units, hence the name isoprenoid pathway. Enzymatic combination of isoprene units leads to the thirty-carbon squalene molecule, which is 10 the penultimate precursor to sterols.

Throughout plants, animals, and fungus, the reactions proceed as: acetyl CoA _ HMGCoA, mevalonate, mevalonate 5 phosphate, mevalonate 5-pyrophosphate, isopentyl diphosphate, 5-pyrophosphatemevalonate, isopentyl pyrophosphate (PIP), dimethylallyl pyrophosphate (DMAPP), PIP + DMAPP, geranyl pyrophosphate + IPP, farnesyl pyrophosphate, 15 2 farnesyl pyrophosphate, squalene and squalene epoxide

From squalene epoxide, the sterol biosynthesis pathway of plants diverges from that of animals and fungi. In plants, cycloartenol is produced next by cyclization of squalene epoxide. The plant pathway eventually leads to the synthesis of the predominant phytosterol, sitosterol.

Animals go on to produce lanosterol from squalene epoxide, eventually leading to 20 cholesterol, which is the precursor to steroid hormones and bile acids, among other compounds. In fungi, lanosterol leads to the production of the predominant sterol, ergosterol.

An important regulatory control step within the pathway consists of the HMGCoA _ Mevalonate step, catalyzed by HMGCoA reductase, and the condensation of 2 farnesyl pyrophosphates _ squalene, catalyzed by squalene synthase. An early, reported rate-limiting 25 step, in the pathway is the HMGCoA reductase-catalyzed reaction.

A number of studies have focused on the regulation of HMGCoA reductase. HMGCoA reductase (EC 1.1.1.34) catalyzes the reductive conversion of HMGCoA to mevalonic acid

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(MVA). This reaction is a reported controlling step in isoprenoid biosynthesis. The enzyme is regulated by feedback mechanisms and by a system of activation kinases and phosphatases (Gray, *Adv. Bot. Res.*, *14*: 25 (1987); Bach *et al.*, *Lipids*, 26: 637 (1991); Stermer *et al.*, *J. Lipid Res.*, 35: 1133 (1994), all of which are herein incorporated by reference in their entirety).

5        Another important regulation occurs at the squalene synthase step. Squalene synthase (EC 2.5.1.21) reductively condenses two molecules of FPP in the presence of $Mg^{2+}$ and NADPH to form squalene. The reaction involves a head-to-head condensation and forms a stable intermediate, presqualene diphosphate. The enzyme is subject to regulation similar to that of HMGCoA reductase and acts by balancing the incorporation of FPP into sterols and other

10     compounds.

The sterol pathway of plants diverges from that in animals and fungi after squalene epoxide. In plants, the cyclization of squalene epoxide occurs next, under the regulated control of cycloartenol synthase (EC 5.4.99.8). The cyclization mechanism proceeds from the epoxy end into a chair-boat-chair-boat sequence that is mediated by a transient C-20 carbocationic

15     intermediate. The reported rate-limiting step in plant sterol synthesis occurs in the next step, S-adenosyl-L-methionine:sterol C-24 methyl transferase (EC 2.1.1.41) ($SMT_I$) catalyzing the transfer of a methyl group from a cofactor, S-adenosyl-L-methionine, to the C-24 center of the sterol side chain. This is the first of two methyl transfer reactions. The second methyl transfer reaction occurs further down in the pathway and has been reported to be catalyzed by $SMT_{II}$. An

20     isoform enzyme, $SMT_{II}$, catalyzes the conversion of 24-methylene lophenol to 24-ethylidene lophenol (Fonteneau *et al.*, *Plant Sci Lett* 10:147-155(1977), the entirety of which is herein incorporated by reference). The presence of two distinct SMTs in plants were further confirmed by cloning cDNAs code the enzymes from *Arabidopsis* (Husselstein *et al.*, *FEBS Lett* 381:87-92(1996), the entirety of which is herein incorporated by reference), soybean (Shi *et al.*, *J Biol*

25     *Chem* 271: 9384-9389(1996), the entirety of which is herein incorporated by reference), maize (Grebenok *et al.*, *Plant Mol Biol* 34: 891-896(1997), the entirety of which is herein incorporated by reference) and tobacco (Bouvier-Nave *et al.*, *Eur J Biochem* 246: 518-529 (1997); Bouvier-

Nave *et al., Eur J Biochem* 256: 88-96(1998), both of which are herein incorporated by reference in their entirety).

Later in the pathway, a sterol C-14 demethylase catalyzes the demethylation at C-14, removing the methyl group and creating a double bond. Interestingly, this enzyme also occurs in plants and fungi, but at a different point in the pathway. Sterol C14-demethylation is mediated by a cytochrome P-450 complex. A large family of enzymes utilize the cytochrome P-450 complex. There is, in addition, a family of cytochrome P450 complexes. For example, sterol C-22 desaturase (EC 2.7.3.9) catalyzes the formation of the double bond at C-22 on the side chain. The C-22 desaturase in yeast, which is the final step in the biosynthesis of ergosterol, contains a cytochrome P450 that is distinct from the cytochrome P450 participating in the demethylation reaction. Additional cytochrome P450 enzymes participate in brassinosteroid synthesis (Bishop, *Plant Cell* 8:959-969 (1996), the entirety of which is herein incorporated by reference). Brassinosteroids are steroidal compounds with plant growth regulatory properties, including modulation of cell expansion and photomorphogenesis (Artecal, *Plant Hormones, Physiology, Biochemistry and Molecular Biology* ed. Davies, Kluwer Academic Publishers, Dordrecht, 66 (1995), Yakota, *Trends in Plant Science* 2:137-143 (1997), both of which are herein incorporated by reference in their entirety).

One class of proteins, oxysterol-binding proteins, have been reported in humans and yeast (Jiang *et al., Yeast 10:* 341-353 (1994), the entirety of which is herein incorporated by reference). These proteins have been reported to modulate ergosterol levels in yeast (Jiang *et al., Yeast 10:* 341-353 (1994)). In particular, Jiang *et al.,* reported three genes KES1, HES1 and OSH1, which encode proteins containing an oxysterol-binding region.

**Enzyme Inhibitors and Modulators**

Self-regulatory and feedback regulatory mechanisms of some of the sterol synthesis enzymes provide opportunities to effect sterol metabolism. For example, the introduction of the feedback inhibitor molecule inhibits enzyme action while the removal of that molecule up-regulates the enzyme. In certain circumstances, non-wild type enzymes can effect normal

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regulation. These organisms can be generated, for example, by traditional genetic crosses, mutation treatments and through molecular genetics. One example is the overexpression of plant HMGCoA reductase in transgenic plants resulting in a 6-10 fold increase in the total sterol levels (for example, transgenic tobacco plants overproducing phytosterols in Schaller *et al., Plant*

5    *Physiol. 109*: 761 (1995), the entirety of which is herein incorporated by reference).

A number of compounds have been identified that, at least partially, exert their effects on sterol synthesis. For example, mevinolinic acid and lovastatin are competitive inhibitors of HMGCoA reductase and zaragonic acid is a competitive inhibitor of squalene synthase (Alberts *et al., Proc. Natl. Acad. Sci. (U.S.A.)* 77:3957-61 (1993); Bergstrom *et al., Proc. Natl. Acad. Sci.*

10   *(U.S.A.)* 90:80-84 (1980), both of which are herein incorporated by reference). Many fungicides and insecticides act by inhibiting enzymes, such as those noted above or the C-14 demethylase enzyme (*Sterol Biosynthesis Inhibitors and* Anti-feeding Compounds, Kato *et al.*, Springer-Verlag, New York (1986); *Sterol biosynthesis inhibitors: pharmaceutical and agrochemical aspects*, eds. Berg and Plempel, Ellis Horwood, Chichester, England (1988), both of which are

15   herein incorporated by reference in this entirety).

However, the use of these compounds can have toxic effects that preclude their use in products destined for animal or human consumption. Furthermore, the increase or decrease in sterol levels possible using these compounds is limited. Typically, the changes in levels occur over a wide spectrum of the pathway. New and more effective methods for manipulating sterol

20   synthesis are desired.

The present invention provides a gene, *Hes1*, involved in plant phytosterol production. Expression of HES1 (protein) in organisms such as plants can increase phytosterol biosynthesis. The present invention also provides transgenic organisms expressing a HES1 protein, which can enhance food and feed sources.

25                                    **SUMMARY OF THE INVENTION**

The present invention includes a substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 622.

The present invention includes a substantially purified nucleic acid molecule that specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 1 or its complement, wherein the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO: 622.

5    The present invention includes a substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 623.

The present invention includes a substantially purified nucleic acid molecule that specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 2 or its complement, wherein the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO:

10    623.

The present invention includes a substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 624.

The present invention includes a substantially purified nucleic acid molecule that specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 3 or its complement, wherein

15    the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO:

624.

The present invention includes a substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 625.

The present invention includes a substantially purified nucleic acid molecule that

20    specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 4 or its complement, wherein the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO:

625.

The present invention includes a substantially purified nucleic acid molecule comprising a nucleic acid sequence which encodes a plant HES1 protein.

25    The present invention includes an antibody capable of specifically binding a protein comprising the amino acid sequence of SEQ ID NO: 622.

The present invention includes an antibody capable of specifically binding a protein comprising the amino acid sequence of SEQ ID NO: 623.

The present invention includes an antibody capable of specifically binding a protein comprising the amino acid sequence of SEQ ID NO: 624.

5          The present invention includes an antibody capable of specifically binding a protein comprising the amino acid sequence of SEQ ID NO: 625.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a structural nucleic acid molecule,

10     wherein the structural nucleic acid molecule comprises a nucleic acid sequence encoding a protein having an amino acid sequence selected from the group consisting of SEQ ID NO: 622 through SEQ ID NO: 626 or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

15     The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to (B) a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule comprising a nucleic acid sequence selected from the

20     group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in plant cells to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a method for determining a level or pattern in a plant of a protein in a plant comprising: (A) incubating, under conditions permitting nucleic acid

25     hybridization, a marker nucleic acid molecule, the marker nucleic acid molecule selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having the nucleic acid sequence of SEQ ID NO: 1 through SEQ ID NO: 621 or

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complements thereof, with a complementary nucleic acid molecule obtained from the plant cell or plant tissue, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant permits the detection of an mRNA for the enzyme; (B) permitting hybridization between the marker nucleic acid molecule

5 and the complementary nucleic acid molecule obtained from the plant cell or plant tissue; and (C) detecting the level or pattern of the complementary nucleic acid, wherein the detection of the complementary nucleic acid is predictive of the level or pattern of the protein in the plant.

The present invention also provides a method for determining a level or pattern of a protein in a plant under evaluation which comprises assaying the concentration of a molecule,

10 whose concentration is dependent upon the expression of a gene, the gene specifically hybridizes to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof, in comparison to the concentration of that molecule present in a reference plant with a known level or pattern of the protein, wherein the assayed concentration of the molecule is compared to the assayed

15 concentration of the molecule in the reference plant with the known level or pattern of the protein.

The present invention also provides a method for determining a mutation in a plant whose presence is predictive of a mutation affecting a level or pattern of a protein comprising the steps: (A) incubating, under conditions permitting nucleic acid hybridization, a marker nucleic acid,

20 the marker nucleic acid selected from the group of marker nucleic acid molecules which specifically hybridize to a nucleic acid molecule having a nucleic acid sequence selected from the group of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof and a complementary nucleic acid molecule obtained from the plant, wherein nucleic acid hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the

25 plant permits the detection of a polymorphism whose presence is predictive of a mutation affecting the level or pattern of the protein in the plant; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the

plant; and (C) detecting the presence of the polymorphism, wherein the detection of the polymorphism is predictive of the mutation.

The present invention also provides a method of producing a plant containing an overexpressed protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region has a nucleic acid sequence selected from group consisting of SEQ ID NO: 1 through SEQ ID NO: 621, wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the protein; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing an overexpressed protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region encodes a protein comprising an amino acid sequence selected from group consisting of SEQ ID NO: 622 through SEQ ID NO: 626, wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in overexpression of the protein; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing reduced levels of a protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region comprises a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of

polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in co-suppression of the protein; and (B) growing the transformed plant.

The present invention also provides a method of producing a plant containing reduced levels of a protein comprising: (A) transforming the plant with a functional nucleic acid molecule, wherein the functional nucleic acid molecule comprises a promoter region, wherein the promoter region is linked to a structural region, wherein the structural region encodes a protein comprising an amino acid sequence selected from group consisting of SEQ ID NO: 622 through SEQ ID NO: 626; wherein the structural region is linked to a 3' non-translated sequence that functions in the plant to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and wherein the functional nucleic acid molecule results in co-suppression of the protein; and (B) growing the transformed plant.

The present invention also provides a method for reducing expression of a protein in a plant comprising: (A) transforming the plant with a nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule, wherein the exogenous promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or fragments thereof and the transcribed strand is complementary to an endogenous mRNA molecule; and wherein the transcribed nucleic acid molecule is linked to a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and (B) growing the transformed plant.

The present invention also provides a method for reducing expression of a protein in a plant comprising: (A) transforming the plant with a nucleic acid molecule, the nucleic acid molecule having an exogenous promoter region which functions in a plant cell to cause the

production of a mRNA molecule, wherein the exogenous promoter region is linked to a transcribed nucleic acid molecule having a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule having a nucleic acid encodes a protein comprising an amino acid sequence selected from group consisting of SEQ ID NO: 622 through SEQ ID NO: 626 or frgaments thereof and the transcribed strand is complementary to an endogenous mRNA molecule; and wherein the transcribed nucleic acid molecule is linked to a 3' non-translated sequence that functions in the plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of a mRNA molecule; and (B) growing the transformed plant.

The present invention also provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule has a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragment of either; and (B) calculating the degree of association between the polymorphism and the plant trait.

The present invention also provides a method of isolating a nucleic acid that encodes a protein or fragment thereof comprising: (A) incubating under conditions permitting nucleic acid hybridization, a first nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragment of either with a complementary second nucleic acid molecule obtained from a plant; (B) permitting hybridization between the first nucleic acid molecule and the second nucleic acid molecule obtained from the plant; and (C) isolating the second nucleic acid molecule.

The present invention also provides a method for producing a protein or fragment thereof in an organism comprising introducing a vector comprising a nucleic acid of the present invention and expressing the protein or fragment.

## DETAILED DESCRIPTION OF THE INVENTION

One skilled in the art can refer to general reference texts for detailed descriptions of known techniques discussed herein or equivalent techniques. These texts include *Current Protocols in Molecular Biology* Ausubel, *et al.,* eds., John Wiley & Sons, N.Y. (1989), and supplements through September (1998), *Molecular Cloning, A Laboratory Manual* (Sambrook *et al.,* 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), for example, each of which are specifically incorporated by reference in their entirety). These texts can also be referred to in making or using an aspect of the invention.

The agents of the invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic and thus involve the capacity of the agent to mediate a chemical reaction or response.

The term "substantially purified", as used herein, refers to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the invention may also be recombinant. As used herein, the term recombinant means any agent (*e.g.*, DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

It is understood that the agents of the invention may be labeled with reagents that facilitate detection of the agent (*e.g.*, fluorescent labels, Prober *et al., Science 238*:336-340 (1987); Albarella *et al.,* EP 144914; chemical labels, Sheldon *et al.,* U.S. Patent 4,582,789; Albarella *et al.,* U.S. Patent 4,563,417; modified bases, Miyoshi *et al.,* EP 119448, all of which

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are hereby incorporated by reference in their entirety). It is further understood that the invention provides recombinant bacterial, mammalian, microbial, archaebacterial, insect, fungal, and plant cells as well as viral constructs comprising the agents of the invention.

### (a) Nucleic Acid Molecules

Agents of the invention include nucleic acid molecules and, more preferably, nucleic acid molecules of maize, soybean, canola, yeast, or *Arabidopsis*. In addition, a number of different plants can be the ultimate source of the nucleic acid molecules of the invention. An exemplary group of genotypes includes: B73 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.); B73 x Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.); DK604 (Dekalb Genetics, Dekalb, Illinois U.S.A.); H99 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.); RX601 (Asgrow Seed Company, Des Moines, Iowa); and Mo17 (Illinois Foundation Seeds, Champaign, Illinois U.S.A.). And an exemplary group of soybean types includes: Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa); C1944 (United States Department of Agriculture (USDA) Soybean Germplasm Collection, Urbana, Illinois U.S.A.); Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.); FT108 (Monsoy, Brazil); Hartwig (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.); BW211S Null (Tohoku University, Morioka, Japan), PI507354 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.); Asgrow A4922 (Asgrow Seed Company, Des Moines, Iowa U.S.A.); PI227687 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.); PI229358 (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.); and Asgrow A3237 (Asgrow Seed Company, Des Moines, Iowa U.S.A.).

A particularly preferred embodiment of the nucleic acid molecules of the present invention are plant nucleic molecules that comprise a nucleic acid sequence which encodes an oxysterol-binding protein consensus sequence, for example, soybean HES1 (SEQ ID NOS: 622, 623 and 624), and maize HES1 (SEQ ID NO: 625).

Another particularly preferred embodiment of the nucleic acid molecules of the present invention are yeast nucleic acid molecules that comprise a nucleic acid sequence which encodes an oxysterol-binding protein consensus sequence, for example yeast HES1 (SEQ ID NO: 626).

A particularly preferred embodiment of the nucleic acid molecules of the invention are
5  nucleic acid molecules that encode a protein or fragment thereof where the protein or fragment thereof is selected from the group consisting of a HES1, HMGCoA reductase, squalene synthase, cycloartenol synthase, SMTI, SMTII and UPC2. In a more particularly preferred embodiment of the nucleic acid molecules of the present invention are nucleic acid molecules that encode a protein or fragment thereof where the protein or fragment thereof is selected from the group
10 consisting of a fungal, more preferably a yeast HES1, a plant, more preferably a maize, soybean or *Arabidopsis* HES1, a plant, more preferably a rubber or an *Arabidopsis* HMGCoA reductase, a plant, more preferably an *Arabidopsis* squalene synthase, a plant, more preferably an *Arabidopsis* cycloartenol synthase, a plant, more preferably an *Arabidopsis* SMTI or SMTII and a fungus, more preferably a yeast UPC2.

15 In a preferred embodiment, the nucleic molecule encodes a HES1 protein, preferably a plant HES1 protein comprising an oxysterol-binding protein consensus sequence -- E(K, Q) xSH (H, R) PPx (S, T, A, C, F)A. In a further preferred embodiment, the nucleic acid molecule encodes a HES1 protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID NO: 625. In a further
20 preferred embodiment, the nucleic acid molecule molecules encodes a HES1 protein with a conservative amino acid substitution in an amino acid sequence selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID NO: 625. In a further preferred embodiment, the nucleic acid molecule molecules encodes a HES1 protein with between 2 and 5 conservative amino acid substitutions in an amino acid sequence selected from
25 the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID NO: 625. In a further preferred embodiment, the nucleic acid molecule molecules encodes a HES1 protein with between 5 and 10 conservative amino acid substitutions in an amino acid sequence

selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and

SEQ ID NO: 625. In a further preferred embodiment, the nucleic acid molecule encodes a HES1

protein with more than 10 conservative amino acid substitutions in an amino acid sequence

selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and

5    SEQ ID NO: 625.

In another preferred embodiment, the nucleic molecule encodes a HES1 protein,

preferably a yeast HES1 protein comprising an oxysterol-binding protein consensus sequence --

E(K, Q) xSH (H, R) PPx (S, T, A, C, F)A. In a further preferred embodiment, the nucleic acid

molecule encodes a HES1 protein comprising an amino acid sequence SEQ ID NO: 626. In a

10   further preferred embodiment, the nucleic acid molecule molecules encodes a HES1 protein with

a conservative amino acid substitution in amino acid sequence SEQ ID NO: 626. In a further

preferred embodiment, the nucleic acid molecule molecules encodes a HES1 protein with

between 2 and 5 conservative amino acid substitutions in an amino acid sequence SEQ ID NO:

626. In a further preferred embodiment, the nucleic acid molecule molecules encodes a HES1

15   protein with between 5 and 10 conservative amino acid substitutions in an amino acid sequence

SEQ ID NO: 626. In a further preferred embodiment, the nucleic acid molecule encodes a HES1

protein with more than 10 conservative amino acid substitutions in an amino acid sequence SEQ

ID NO: 626.

In an aspect of the present invention, one or more of the nucleic acid molecules of the

20   present invention differ in nucleic acid sequence from those encoding a protein or fragment

thereof in SEQ ID NO: 1 through SEQ ID NO: 621 due to the degeneracy in the genetic code in

that they encode the same protein but differ in nucleic acid sequence. In another further aspect of

the present invention, one or more of the nucleic acid molecules of the present invention differ in

nucleic acid sequence from those encoding a protein or fragment thereof in SEQ ID NO: 1

25   through SEQ ID NO: 621 due to fact that the different nucleic acid sequence encodes a protein

having one or more conservative amino acid residue. Examples of conservative substitutions are

set forth in Table 1. It is understood that codons capable of coding for such conservative substitutions are known in the art.

**Table 1**

| Original Residue | Conservative Substitutions |
|---|---|
| Ala | Ser |
| Arg | Lys |
| Asn | Gln; His |
| Asp | Glu |
| Cys | Ser; Ala |
| Gln | Asn |
| Glu | Asp |
| Gly | Pro |
| His | Asn; Gln |
| Ile | Leu; Val |
| Leu | Ile; Val |
| Lys | Arg; Gln; Glu |
| Met | Leu; Ile |
| Phe | Met; Leu; Tyr |
| Ser | Thr |
| Thr | Ser |
| Trp | Tyr |
| Tyr | Trp; Phe |
| Val | Ile; Leu |

In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a protein or fragment thereof set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or fragment thereof due to the fact

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that one or more codons encoding an amino acid has been substituted for a codon that encodes a nonessential substitution of the amino acid originally encoded.

One subset of the nucleic acid molecules of the invention is fragment nucleic acids molecules. Fragment nucleic acid molecules may consist of significant portion(s) of, or indeed most of, the nucleic acid molecules of the invention, such as those specifically disclosed. Alternatively, the fragments may comprise smaller oligonucleotides (having from about 15 to about 400 nucleotide residues and more preferably, about 15 to about 30 nucleotide residues, or about 50 to about 100 nucleotide residues, or about 100 to about 200 nucleotide residues, or about 200 to about 400 nucleotide residues, or about 275 to about 350 nucleotide residues).

A fragment of one or more of the nucleic acid molecules of the invention may be a probe and specifically a PCR probe. A PCR probe is a nucleic acid molecule capable of initiating a polymerase activity while in a double-stranded structure with another nucleic acid. Various methods for determining the structure of PCR probes and PCR techniques exist in the art. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STS_Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques* 25:112-123 (1998)), for example, can be used to identify potential PCR primers.

As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure.

A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit

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them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual, 2nd Ed., Cold Spring Harbor Press*, Cold Spring Harbor, New York (1989) and by Haymes *et al.*, *Nucleic Acid Hybridization, A Practical Approach, IRL Press*,

5      Washington, DC (1985). Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

10      Appropriate stringency conditions which promote DNA hybridization are, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 20-25°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 X SSC at 50°C to a high stringency

15      of about 0.2 X SSC at 65°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

In a preferred embodiment, a nucleic acid of the invention will specifically hybridize to

20      one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or more preferably to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4, SEQ ID NO: 6 through SEQ ID NO: 29 or complements thereof under moderately stringent conditions, for example at about 2.0 X SSC and about 65°C.

25      In a particularly preferred embodiment, a nucleic acid of the invention will include those nucleic acid molecules that specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or more preferably

to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4, SEQ ID NO: 6 through SEQ ID NO: 29 or complements thereof under high stringency conditions such as 0.2 X SSC and about 65°C.

In one aspect of the invention, the nucleic acid molecules of the invention have one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragment thereof or more preferably to a nucleic acid molecule having SEQ ID NO: 1 through SEQ ID NO: 4, SEQ ID NO: 6 through SEQ ID NO: 29 or complements thereof. In another aspect of the invention, one or more of the nucleic acid molecules of the invention share between about 100% and 70% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or more preferably to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4, SEQ ID NO: 6 through SEQ ID NO: 29 or complements thereof. In a further aspect of the invention, one or more of the nucleic acid molecules of the invention share between about 100% and 90% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or more preferably to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4, SEQ ID NO: 6 through SEQ ID NO: 29 or complements thereof. In a more preferred aspect of the invention, one or more of the nucleic acid molecules of the invention share between about 100% and 95% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or more preferably to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4, SEQ ID NO: 6 through SEQ ID NO: 29 or complements thereof. In an even more preferred aspect of the invention, one or more of the nucleic acid molecules of the invention share between about 100% and 99% sequence identity with one or more of the sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or more preferably to a nucleic acid molecule having a nucleic acid sequence selected from the group

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consisting of SEQ ID NO: 1 through SEQ ID NO: 4, SEQ ID NO: 6 through SEQ ID NO: 29, or complements thereof.

In a preferred embodiment the percent identity calculations are performed using the Megalign program of the LASERGENE bioinformatics computing suite (default parameters, DNASTAR Inc., Madison, Wisconsin).

In a preferred embodiment of the present invention, the nucleic acid molecule of the present invention encodes a protein or fragment thereof, where a protein exhibits a BLAST probability score of greater than 1E-12, preferably a BLAST probability score of between about 1E-30 and about 1E-12, even more preferably a BLAST probability score of greater than 1E-30 with its homologue.

In a preferred embodiment of the present invention, the nucleic molecule of the present invention encodes a protein or fragment thereof where a protein exhibits a BLAST score of greater than 120, preferably a BLAST score of between about 1450 and about 120, even more preferably a BLAST score of greater than 1450 with its homologue.

Nucleic acid molecules of the present invention can comprise sequences that encode a protein or fragment thereof. Such proteins or fragments thereof include homologues of known proteins in other organisms.

A nucleic acid molecule of the invention can also encode a homolog protein. As used herein, a homolog protein molecule or fragment thereof is a counterpart protein molecule or fragment thereof in a second species (*e.g.*, maize HES1 is a homolog of *Arabidopsis* HES1). A homolog can also be generated by molecular evolution or DNA shuffling techniques, so that the molecule retains at least one functional or structure characteristic of the original protein (*see*, for example, U.S. Patent 5,811,238).

Particularly preferred homologues are selected from the group consisting of alfalfa, *Arabidopsis,* barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, maize, peanut, pepper, potato, rice, rye, sorghum, soybean, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce,

lentils, grape, banana, tea, turf grasses, sunflower, soybean, and *Phaseolus*. A particularly

preferred group of homologues are crops harvested for seed oils, including but not limited to

rapeseed (high erucic acid rape and canola), maize, soybean, safflower, sunflower, cotton,

peanut, flax, oil palm and Cuphea.

5        In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1 through SEQ

ID NO: 621 or complements and fragments of either can be utilized to obtain such homologues.

The degeneracy of the genetic code, which allows different nucleic acid sequences to

code for the same protein or peptide, is known in the literature. (U.S. Patent No. 4,757,006, the

entirety of which is herein incorporated by reference).

10       Agents of the invention include nucleic acid molecules that encode a substantially

purified nucleic acid molecules encoding at least about a 10 amino acid region, more preferably a

20, 30, 40, or 50 amino acid region, of a protein selected from the group consisting of a fungal,

more preferably a yeast HES1, a plant, more preferably a maize, soybean or *Arabidopsis* HES1, a

plant, more preferably a rubber or an *Arabidopsis* HMGCoA reductase, a plant, more preferably

15       an *Arabidopsis* squalene synthase, a plant, more preferably an *Arabidopsis* cycloartenol synthase,

a plant, more preferably an *Arabidopsis* SMTI or SMTII and a fungus, more preferably a yeast

UPC2.

**(b)    Protein and Peptide Molecules**

A class of agents comprises one or more of the protein or fragments thereof or peptide

20       molecules having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1

through SEQ ID NO: 621 or one or more of the protein or fragment thereof and peptide

molecules encoded by other nucleic acid agents of the invention. A particular preferred class of

proteins are those having an amino acid sequence selected from the group consisting of SEQ ID

NO: 622 through SEQ ID NO: 625 or fragments thereof.

25       As used herein, the term "protein molecule" or "peptide molecule" includes any molecule

that comprises five or more amino acids. It is well known in the art that proteins may undergo

modification, including post-translational modifications, such as, but not limited to, disulfide

bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the

term "protein molecule" or "peptide molecule" includes any protein molecule that is modified by

any biological or non-biological process. The terms "amino acid" and "amino acids" refer to all

naturally occurring L-amino acids. This definition is meant to include norleucine, norvaline,

5    ornithine, homocysteine, and homoserine.

One or more of the protein or fragment of peptide molecules may be produced via

chemical synthesis, or more preferably, by expressing in a suitable bacterial or eukaryotic host.

Suitable methods for expression are described by Sambrook *et al.*, In: *Molecular Cloning, A*

*Laboratory Manual, 2nd Edition, Cold Spring Harbor Press*, Cold Spring Harbor, New York

10   (1989), or similar texts.

A "protein fragment" is a peptide or polypeptide molecule whose amino acid sequence

comprises a subset of the amino acid sequence of that protein. A protein or fragment thereof that

comprises one or more additional peptide regions not derived from that protein is a "fusion"

protein. Such molecules may be derivatized to contain carbohydrate or other moieties (such as

15   keyhole limpet hemocyanin, etc.). Fusion protein or peptide molecules of the invention are

preferably produced via recombinant means.

Another class of agents comprise protein or peptide molecules or fragments or fusions

thereof comprising SEQ ID NO: 622 through SEQ NO: 625 or fragment thereof or encoded by

SEQ ID NO: 1 through SEQ ID NO: 621 in which conservative, non-essential or non-relevant

20   amino acid residues have been added, replaced or deleted. Computerized means for designing

modifications in protein structure are known in the art (Dahiyat and Mayo, *Science* 278:82-87

(1997), the entirety of which is herein incorporated by reference).

A particularly preferred embodiment of the nucleic acid molecules of the present

invention are proteins comprising an amino acid sequence which corresponds to an oxysterol-

25   protein binding consensus sequence.

In a preferred embodiment of the present invention, the nucleic molecule of the present

invention encodes a protein or fragment thereof, where a protein exhibits a BLAST probability

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score of greater than 1E-12, preferably a BLAST probability score of between about 1E-30 and about 1E-12, even more preferably a BLAST probability score of greater than 1E-30 with its homologue.

In a preferred embodiment of the present invention, the nucleic molecule of the present invention encodes a protein or fragment thereof where a protein exhibits a BLAST score of greater than 120, preferably a BLAST score of between about 1450 and about 120, even more preferably a BLAST score of greater than 1450 with its homologue.

In another preferred embodiment of the present invention, the nucleic acid molecule encoding a protein or fragment thereof exhibits a % identity with its homologue of between about 25% and about 40%, more preferably of between about 40 and about 70%, even more preferably of between about 70% and about 90% and even more preferably between about 90% and 99%. In another preferred embodiment of the present invention, a protein or fragments thereof exhibits a % identity with its homologue of 100%.

In a preferred embodiment the percent identity calculations are performed using the Megalign program of the LASERGENE bioinformatics computing suite (default parameters, DNASTAR Inc., Madison, Wisconsin).

A protein of the invention can also be a homologue protein. As used herein, a homologue protein molecule or fragment thereof is a counterpart protein molecule or fragment thereof in a second species (e.g., maize HMGCoA reductase is a homologue of Arabidopsis HMGCoA reductase). A homologue can also be generated by molecular evolution or DNA shuffling techniques, so that the molecule retains at least one functional or structure characteristic of the original (see, for example, U.S. Patent 5,811,238, the entirety of which is herein incorporated by reference).

Particularly preferred homologues are selected from the group consisting of alfalfa, Arabidopsis, barley, Brassica, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, maize, peanut, pepper, potato, rice, rye, sorghum, soybean, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce,

lentils, grape, banana, tea, turf grasses, sunflower, soybean, and *Phaseolus*. A particularly preferred group of homologues are those from oil plants such as cotton, canola and sunflower.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1 through SEQ ID NO: 621 or complements and fragments of either can be utilized to obtain such homologues.

5         The degeneracy of the genetic code, which allows different nucleic acid sequences to code for the same protein or peptide, is known in the literature. (U.S. Patent No. 4,757,006, the entirety of which is herein incorporated by reference).

Agents of the invention include proteins comprising at least about a 10 amino acid region, more preferably a 20, 30, 40, or 50 amino acid region, of a protein selected from the group consisting of a fungal, more preferably a yeast HES1, a plant, more preferably a maize, soybean or *Arabidopsis* HES1, a plant, more preferably a rubber or an *Arabidopsis* HMGCoA reductase, a plant, more preferably an *Arabidopsis* squalene synthase, a plant, more preferably an *Arabidopsis* cycloartenol synthase, a plant, more preferably an *Arabidopsis* SMTI or SMTII and a fungus, more preferably a yeast UPC2.

### (c)     Plant Constructs and Plant Transformants

One or more of the nucleic acid molecules of the invention may be used in plant transformation or transfection. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of being inserted into any organism. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention, preferably a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragments of either. Another preferred class of exogenous genetic material are nucleic acid molecules that encode a protein having an amino acid selected from the group consisting of SEQ ID NO: 622 through SEQ ID NO: 626 or fragments thereof.

Genetic material may be transferred into either monocotyledons and dicotyledons including, but not limited to maize, soybean, *Arabidopsis,* phaseolus, peanut, alfalfa, wheat, rice,

oat, sorghum, rye, tritordeum, millet, fescue, perennial ryegrass, sugarcane, cranberry, papaya, banana, banana, muskmelon, apple, cucumber, dendrobium, gladiolus, chrysanthemum, liliacea, cotton, eucalyptus, sunflower, canola, turfgrass, sugarbeet, coffee and dioscorea (Christou, In: *Particle Bombardment for Genetic Engineering of Plants*, Biotechnology Intelligence Unit, Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference). In a particular preferred embodiment, any seed-bearing plant may be employed as the target plant species for modification in accordance with this invention, including angiosperms, gymnosperms, monocotyledons, and dicotyledons. Plants of special interest are crops harvested for seed oils, including but not limited to rapeseed (high erucic acid rape and canola), maize, soybean, safflower, sunflower, cotton, peanut, flax, oil palm and Cuphea.

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the invention may be overexpressed in a transformed cell or transformed plant. Such overexpression may be the result of transient or stable transfer of the exogenous genetic material.

In another preferred aspect of the present invention, exogenous genetic material is a nucleic acid molecule that comprises a nucleic acid sequence which encodes a HES1 protein or fragment thereof, more preferably a yeast HES1 protein or fragment thereof, even more preferably a plant HES1 protein or fragment thereof.

In a preferred embodiment, expression or overexpression of a HES1 protein in a plant provides in that plant, relative to an untransformed plant with a similar genetic background, an increased level of phytosterols.

In a preferred embodiment, expression or overexpression of a HES1 protein in a plant provides in that plant, relative to an untransformed plant with a similar genetic background, an altered composition of phytosterols.

In another embodiment, overexpression of a HES1 protein in a plant provides in that plant, relative to an untransformed plant with a similar genetic background, an increased level of a HES1 protein in a plastid.

In another preferred embodiment, overexpression of the HES1 protein in a transformed plant will result in a plant which as a food or feed constituent exhibits an increased ability to act as a cholesterol lowering agent relative to an untransformed plant with a similar genetic background.

In a preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is selected from the group consisting of a HES1, HMGCoA reductase, squalene synthase, cycloartenol synthase, SMTI, SMTII and UPC2. In a more particularly preferred embodiment of the present invention is a protein or fragment thereof, where the protein or fragment thereof is selected from the group consisting of a fungal, more preferably a yeast HES1, a plant, more preferably a maize, soybean or *Arabidopsis* HES1, a plant, more preferably a rubber or an *Arabidopsis* HMGCoA reductase, a plant, more preferably an *Arabidopsis* squalene synthase, a plant, more preferably an *Arabidopsis* cycloartenol synthase, a plant, more preferably an *Arabidopsis* SMTI or SMTII and a plant, more preferably a yeast UPC2.

In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is selected from the group consisting a plant HES1, HMGCoA reductase, squalene synthase, cycloartenol synthase, SMTI, SMTII and yeast UPC2. In a further even more particularly preferred embodiment of the present invention the protein or fragment thereof is a plant HES1. In an additional even more particularly preferred embodiment of the present invention the protein or fragment thereof is a maize, soybean or *Arabidopsis* HES1.

In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is a HES1 protein, preferably a plant HES1 protein comprising an oxysterol-binding protein consensus sequence -- E(K, Q) xSH (H, R) PPx (S, T,

A, C, F)A. In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is a HES1 protein that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID NO: 625. In another preferred embodiment of the present invention, the protein

5    or fragment thereof overexpressed in the transgenic plant is a HES1 protein with a conservative amino acid substitution in an amino acid sequence selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID NO: 625. In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is a HES1 protein with between 2 and 5 conservative amino acid substitutions in

10   an amino acid sequence selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID NO: 625. In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is a HES1 protein with between 5 and 10 conservative amino acid substitutions in an amino acid sequence selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID

15   NO: 625. In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is a HES1 protein with more than 10 conservative amino acid substitutions in an amino acid sequence selected from the group consisting of SEQ ID NO: 622, SEQ ID NO: 623, SEQ ID NO: 624 and SEQ ID NO: 625.

In another preferred embodiment of the present invention, the protein or fragment thereof

20   overexpressed in the transgenic plant is a HES1 protein that comprises an amino acid sequence SEQ ID NO: 626. In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is a HES1 protein with a conservative amino acid substitution in an amino acid sequence SEQ ID NO: 626. In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the

25   transgenic plant is a HES1 protein with between 2 and 5 conservative amino acid substitutions in an amino acid sequence SEQ ID NO: 626. In another preferred embodiment of the present invention, the protein or fragment thereof overexpressed in the transgenic plant is a HES1 protein

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with between 5 and 10 conservative amino acid substitutions in an amino acid sequence SEQ ID

NO: 625. In another preferred embodiment of the present invention, the protein or fragment

thereof overexpressed in the transgenic plant is a HES1 protein with more than 10 conservative

amino acid substitutions in an amino acid sequence SEQ ID NO: 626.

5          Exogenous genetic material may be transferred into a host cell by the use of a DNA

vector or construct designed for such a purpose. Design of such a vector is generally within the

skill of the art *(See, Plant Molecular Biology: A Laboratory Manual*, Clark (ed.), Springier, New

York (1997), the entirety of which is herein incorporated by reference).

          A construct or vector may include a plant promoter to express the protein or protein

10     fragment of choice. A number of promoters, which are active in plant cells, have been described

in the literature. These include the nopaline synthase (NOS) promoter (Ebert *et al., Proc. Natl.*

*Acad. Sci. (U.S.A.) 84*:5745-5749 (1987), the entirety of which is herein incorporated by

reference), the octopine synthase (OCS) promoter (which are carried on tumor-inducing plasmids

of *Agrobacterium tumefaciens*), the caulimovirus promoters such as the cauliflower mosaic virus

15     (CaMV) 19S promoter (Lawton *et al., Plant Mol. Biol. 9*:315-324 (1987), the entirety of which is

herein incorporated by reference) and the CaMV 35S promoter (Odell *et al., Nature 313*:810-812

(1985), the entirety of which is herein incorporated by reference), the figwort mosaic virus 35S-

promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate

carboxylase (ssRUBISCO), the Adh promoter (Walker *et al., Proc. Natl. Acad. Sci. (U.S.A.)*

20     *84*:6624-6628 (1987), the entirety of which is herein incorporated by reference), the sucrose

synthase promoter (Yang *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87*:4144-4148 (1990), the entirety

of which is herein incorporated by reference), the R gene complex promoter (Chandler *et al., The*

*Plant Cell 1*:1175-1183 (1989), the entirety of which is herein incorporated by reference) and the

chlorophyll a/b binding protein gene promoter, etc. These promoters have been used to create

25     DNA constructs that have been expressed in plants; *see, e.g.*, PCT publication WO 84/02913,

herein incorporated by reference in its entirety. The CaMV 35S promoters are preferred for use

in plants. Promoters known or found to cause transcription of DNA in plant cells can be used in the invention.

For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized have relatively high expression in these specific tissues. Tissue-specific expression of a protein of the present invention is a particularly preferred embodiment. For this purpose, one may choose from a number of promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea (Edwards *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 87:3459-3463 (1990), herein incorporated by reference in its entirety), the chloroplast fructose-1,6-biphosphatase (FBPase) promoter from wheat (Lloyd *et al.*, *Mol. Gen. Genet.* 225:209-216 (1991), herein incorporated by reference in its entirety), the nuclear photosynthetic ST-LS1 promoter from potato (Stockhaus *et al.*, *EMBO J.* 8:2445-2451 (1989), herein incorporated by reference in its entirety), the serine/threonine kinase (PAL) promoter and the glucoamylase (CHS) promoter from *Arabidopsis thaliana.* Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, cab6, from pine (Yamamoto *et al.*, *Plant Cell Physiol.* 35:773-778 (1994), herein incorporated by reference in its entirety), the promoter for the Cab-1 gene from wheat (Fejes *et al.*, *Plant Mol. Biol.* 15:921-932 (1990), herein incorporated by reference in its entirety), the promoter for the CAB-1 gene from spinach (Lubberstedt *et al.*, *Plant Physiol.* 104:997-1006 (1994), herein incorporated by reference in its entirety), the promoter for the cab1R gene from rice (Luan *et al.*, *Plant Cell.* 4:971-981 (1992), the entirety of which is herein incorporated by reference), the pyruvate, orthophosphate dikinase (PPDK) promoter from maize (Matsuoka *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 90: 9586-9590 (1993), herein incorporated by reference in its entirety), the promoter for the tobacco Lhcb1*2 gene (Cerdan *et al.*, *Plant Mol. Biol.* 33:245-255 (1997), herein incorporated by reference in its entirety), the *Arabidopsis thaliana* SUC2 sucrose-H+ symporter promoter (Truernit *et al.*, *Planta.* 196:564-570 (1995), herein incorporated by reference in its

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entirety) and the promoter for the thylakoid membrane proteins from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other promoters for the chlorophyll a/b-binding proteins may also be utilized in the invention, such as the promoters for LhcB gene and PsbP gene from white mustard (*Sinapis alba*; Kretsch *et al.*, *Plant Mol. Biol.* *28*:219-229 (1995), the entirety of which

5     is herein incorporated by reference).

For the purpose of expression in sink tissues of the plant, such as the tuber of the potato plant, the fruit of tomato, or the seed of maize, wheat, rice and barley, it is preferred that the promoters utilized in the invention have relatively high expression in these specific tissues. A number of promoters for genes with tuber-specific or -enhanced expression are known, including

10    the class I patatin promoter (Bevan *et al.*, *EMBO J.* *8*:1899-1906 (1986); Jefferson *et al.*, *Plant Mol. Biol.* *14*:995-1006 (1990), both of which are herein incorporated by reference in their entirety), the promoter for the potato tuber ADPGPP genes, both the large and small subunits, the sucrose synthase promoter (Salanoubat and Belliard, *Gene 60*:47-56 (1987), Salanoubat and Belliard, *Gene 84*:181-185 (1989), both of which are incorporated by reference in their entirety),

15    the promoter for the major tuber proteins including the 22 kd protein complexes and proteinase inhibitors (Hannapel, *Plant Physiol.* *101*:703-704 (1993), herein incorporated by reference in its entirety), the promoter for the granule bound starch synthase gene (GBSS) (Visser *et al.*, *Plant Mol. Biol.* *17*:691-699 (1991), herein incorporated by reference in its entirety) and other class I and II patatins promoters (Koster-Topfer *et al.*, *Mol Gen Genet.* *219*:390-396 (1989); Mignery *et*

20    *al.*, *Gene.* *62*:27-44 (1988), both of which are herein incorporated by reference in their entirety).

Other promoters can also be used to express a protein or fragment thereof in specific tissues, such as seeds or fruits. The promoter for β-conglycinin (Chen *et al.*, *Dev. Genet. 10*: 112-122 (1989), herein incorporated by reference in its entirety) or other seed-specific promoters such as the napin and phaseolin promoters, can be used. The zeins are a group of storage

25    proteins found in maize endosperm. Genomic clones for zein genes have been isolated (Pedersen *et al.*, *Cell 29*:1015-1026 (1982), herein incorporated by reference in its entirety) and the promoters from these clones, including the 15 kD, 16 kD, 19 kD, 22 kD, 27 kD and γ genes,

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could also be used. Other promoters known to function, for example, in maize include the promoters for the following genes: *waxy, Brittle, Shrunken 2*, Branching enzymes I and II, starch synthases, debranching enzymes, oleosins, glutelins and sucrose synthases. A particularly preferred promoter for maize endosperm expression is the promoter for the glutelin gene from

5      rice, more particularly the Osgt-1 promoter (Zheng *et al., Mol. Cell Biol. 13*:5829-5842 (1993), herein incorporated by reference in its entirety). Examples of promoters suitable for expression in wheat include those promoters for the ADPglucose pyrosynthase (ADPGPP) subunits, the granule bound and other starch synthase, the branching and debranching enzymes, the embryogenesis-abundant proteins, the gliadins and the glutenins. Examples of such promoters in

10     rice include those promoters for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases and the glutelins. A particularly preferred promoter is the promoter for rice glutelin, Osgt-1. Examples of such promoters for barley include those for the ADPGPP subunits, the granule bound and other starch synthase, the branching enzymes, the debranching enzymes, sucrose synthases, the hordeins, the

15     embryo globulins and the aleurone specific proteins.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac *et al., Plant Mol. Biol. 25*:587-596 (1994), the entirety of which is herein incorporated by reference). Expression in root tissue could also be accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have

20     been identified (Lam *et al., Proc. Natl. Acad. Sci. (U.S.A.) 86*:7890-7894 (1989), herein incorporated by reference in its entirety). Other root cell specific promoters include those reported by Conkling *et al.* (Conkling *et al., Plant Physiol. 93*:1203-1211 (1990), the entirety of which is herein incorporated by reference).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos.

25     5,378,619; 5,391,725; 5,428,147; 5,447,858; 5,608,144; 5,608,144; 5,614,399; 5,633,441; 5,633,435; and 4,633,436, all of which are herein incorporated in their entirety. In addition, a

tissue specific enhancer may be used (Fromm *et al.*, *The Plant Cell 1*:977-984 (1989), the entirety of which is herein incorporated by reference).

Constructs or vectors may also include, with the coding region of interest, a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. A number of

5    such sequences have been isolated, including the Tr7 3' sequence and the NOS 3' sequence (Ingelbrecht *et al.*, *The Plant Cell 1*:671-680 (1989), the entirety of which is herein incorporated by reference; Bevan *et al.*, *Nucleic Acids Res. 11*:369-385 (1983), the entirety of which is herein incorporated by reference).

A vector or construct may also include regulatory elements. Examples of such include

10   the Adh intron 1 (Callis *et al.*, *Genes and Develop. 1*:1183-1200 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase intron (Vasil *et al.*, Plant Physiol. 91:1575-1579 (1989), the entirety of which is herein incorporated by reference) and the TMV omega element (Gallie *et al.*, *The Plant Cell 1*:301-311 (1989), the entirety of which is herein incorporated by reference). These and other regulatory elements may be included when

15   appropriate.

A vector or construct may also include a selectable marker. Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to: a neo gene (Potrykus *et al.*, *Mol. Gen. Genet. 199*:183-188 (1985), the entirety of which is herein incorporated by reference), which codes for

20   kanamycin resistance and can be selected for using kanamycin, G418, etc.; a bar gene which codes for bialaphos resistance; a mutant EPSP synthase gene (Hinchee *et al.*, *Bio/Technology 6*:915-922 (1988), the entirety of which is herein incorporated by reference) which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil (Stalker *et al.*, *J. Biol. Chem. 263*:6310-6314 (1988), the entirety of which is herein incorporated by reference); a

25   mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204 (Sept. 11, 1985), the entirety of which is herein

incorporated by reference); and a methotrexate resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem.* *263*:12500-12508 (1988), the entirety of which is herein incorporated by reference).

A vector or construct may also include a transit peptide. Incorporation of a suitable chloroplast transit peptide may also be employed (European Patent Application Publication Number 0218571, the entirety of which is herein incorporated by reference). Translational enhancers may also be incorporated as part of the vector DNA. DNA constructs could contain one or more 5' non-translated leader sequences which may serve to enhance expression of the gene products from the resulting mRNA transcripts. Such sequences may be derived from the promoter selected to express the gene or can be specifically modified to increase translation of the mRNA. Such regions may also be obtained from viral RNAs, from suitable eukaryotic genes, or from a synthetic gene sequence. For a review of optimizing expression of transgenes, see Koziel *et al.*, *Plant Mol. Biol.* *32*:393-405 (1996), the entirety of which is herein incorporated by reference.

A vector or construct may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include: a β-glucuronidase or uidA gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, *Plant Mol. Biol, Rep.* *5*:387-405 (1987), the entirety of which is herein incorporated by reference; Jefferson *et al.*, *EMBO J.* *6*:3901-3907 (1987), the entirety of which is herein incorporated by reference); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues (Dellaporta *et al.*, Stadler Symposium *11*:263-282 (1988), the entirety of which is herein incorporated by reference); a β-lactamase gene (Sutcliffe *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *75*:3737-3741 (1978), the entirety of which is herein incorporated by reference), a gene which encodes an enzyme for which various chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin); a luciferase gene (Ow *et al.*, *Science* *234*:856-859 (1986), the entirety of which is herein incorporated by reference); a xylE gene (Zukowsky *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *80*:1101-1105 (1983), the entirety of which is herein incorporated by reference) which encodes a catechol dioxygenase

that can convert chromogenic catechols; an α-amylase gene (Ikatu *et al.*, *Bio/Technol.* 8:241-242 (1990), the entirety of which is herein incorporated by reference); a tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol.* 129:2703-2714 (1983), the entirety of which is herein incorporated by reference) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone

5    which in turn condenses to melanin; an α-galactosidase, which will turn a chromogenic α-galactose substrate.

Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be

10    identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible proteins which are detectable, (*e.g.*, by ELISA), small active enzymes which are detectable in extracellular solution (*e.g.*, α-amylase, β-lactamase, phosphinothricin transferase), or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence

15    such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

There are many methods for introducing transforming nucleic acid molecules into plant cells. Suitable methods are believed to include virtually any method by which nucleic acid molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of

20    nucleic acid molecules such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc (Potrykus, *Ann. Rev. Plant Physiol. Plant Mol. Biol.* 42:205-225 (1991), the entirety of which is herein incorporated by reference; Vasil, *Plant Mol. Biol.* 25:925-937 (1994), the entirety of which is herein incorporated by reference). For example, electroporation has been used to transform maize protoplasts

25    (Fromm *et al.*, *Nature* 312:791-793 (1986), the entirety of which is herein incorporated by reference).

Other vector systems suitable for introducing transforming DNA into a host plant cell include but are not limited to binary artificial chromosome (BIBAC) vectors (Hamilton *et al.*, *Gene 200*:107-116 (1997), the entirety of which is herein incorporated by reference); and transfection with RNA viral vectors (Della-Cioppa *et al.*, *Ann. N.Y. Acad. Sci.* (1996), 792

5    (Engineering Plants for Commercial Products and Applications), 57-61, the entirety of which is herein incorporated by reference). Additional vector systems also include plant selectable YAC vectors such as those described in Mullen *et al.*, *Molecular Breeding 4*:449-457 (1988), the entirety of which is herein incorporated by reference).

Technology for introduction of DNA into cells is well known to those of skill in the art.

10   Four general methods for delivering a gene into cells have been described:  (1) chemical methods (Graham and van der Eb, *Virology* 54:536-539 (1973), the entirety of which is herein incorporated by reference); (2) physical methods such as microinjection (Capecchi, *Cell* 22:479-488 (1980), the entirety of which is herein incorporated by reference), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun. 107*:584-587 (1982); Fromm *et al.*, *Proc. Natl.*

15   *Acad. Sci. (U.S.A.) 82*:5824-5828 (1985); U.S. Patent No. 5,384,253, all of which are herein incorporated in their entirety); and the gene gun (Johnston and Tang, *Methods Cell Biol. 43*:353-365 (1994), the entirety of which is herein incorporated by reference); (3) viral vectors (Clapp, *Clin. Perinatol. 20*:155-168 (1993); Lu *et al.*, *J. Exp. Med. 178*:2089-2096 (1993); Eglitis and Anderson, *Biotechniques 6*:608-614 (1988), all of which are herein incorporated in their

20   entirety); and (4) receptor-mediated mechanisms (Curiel *et al.*, *Hum. Gen. Ther. 3*:147-154 (1992), Wagner *et al.*, *Proc. Natl. Acad. Sci. (USA) 89*:6099-6103 (1992), both of which are incorporated by reference in their entirety).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid

25   molecules to plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou (eds.), *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994), the entirety of which is herein incorporated by reference). Non-

biological particles (microprojectiles) that may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly transforming monocots, is that neither the isolation of protoplasts (Cristou *et al., Plant Physiol. 87*:671-674 (1988), the entirety of which is herein incorporated by reference) nor the susceptibility of *Agrobacterium* infection are required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics α-particle delivery system, which can be used to propel particles coated with DNA through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with maize cells cultured in suspension. Gordon-Kamm *et al.,* describes the basic procedure for coating tungsten particles with DNA (Gordon-Kamm *et al., Plant Cell 2*:603-618 (1990), the entirety of which is herein incorporated by reference). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the invention is the helium acceleration PDS-1000/He gun is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California)(Sanford *et al., Technique 3*:3-16 (1991), the entirety of which is herein incorporated by reference).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein one may obtain up to 1000 or more foci of cells transiently expressing a marker gene. The

number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from one to ten and average one to three.

In bombardment transformation, one may optimize the pre-bombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable transformants. Both the physical and biological parameters for bombardment are important in this technology. Physical factors are those that involve manipulating the DNA/microprojectile precipitate or those that affect the flight and velocity of either the macro- or microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment and also the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include the particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 87:8526-8530 (1990); Svab and Maliga, *Proc. Natl. Acad. Sci. (U.S.A.)* 90:913-917 (1993); Staub and Maliga, *EMBO J.* 12:601-606 (1993); U.S. Patents 5, 451,513 and 5,545,818, all of which are herein incorporated by reference in their entirety).

Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue distance and helium pressure. One may also minimize the trauma reduction factors by modifying conditions which influence the physiological state of the recipient cells and which may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration and the subculture stage or cell cycle of the recipient cells may be adjusted for

optimum transformation. The execution of other routine adjustments will be known to those of skill in the art in light of the present disclosure.

*Agrobacterium*-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the

5 need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example the methods described by Fraley *et al., Bio/Technology 3*:629-635 (1985) and Rogers *et al., Methods Enzymol. 153*:253-277 (1987), both of which are herein incorporated by reference in their entirety. Further, the integration of the Ti-DNA is a relatively precise process resulting in

10 few rearrangements. The region of DNA to be transferred is defined by the border sequences and intervening DNA is usually inserted into the plant genome as described (Spielmann *et al., Mol. Gen. Genet. 205*:34 (1986), the entirety of which is herein incorporated by reference).

Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al.,* In: *Plant*

15 *DNA Infectious Agents*, Hohn and Schell (eds.), Springer-Verlag, New York, pp. 179-203 (1985), the entirety of which is herein incorporated by reference). Moreover, technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The vectors described have convenient multi-linker regions flanked

20 by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes and are suitable for present purposes (Rogers *et al., Methods Enzymol. 153*:253-277 (1987)). In addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

25 A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for the

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added structural gene; *i.e.*, a transgenic plant that contains two added genes, one gene at the same

locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be

obtained by sexually mating (selfing) an independent segregant transgenic plant that contains a

single added gene, germinating some of the seed produced and analyzing the resulting plants

5    produced for the gene of interest.

It is also to be understood that two different transgenic plants can also be mated to

produce offspring that contain two independently segregating, exogenous genes. Selfing of

appropriate progeny can produce plants that are homozygous for both added, exogenous genes

that encode a polypeptide of interest. Back-crossing to a parental plant and out-crossing with a

10    non-transgenic plant are also contemplated, as is vegetative propagation.

Transformation of plant protoplasts can be achieved using methods based on calcium

phosphate precipitation, polyethylene glycol treatment, electroporation and combinations of these

treatments (*See, for example*, Potrykus *et al.*, *Mol. Gen. Genet. 205*:193-200 (1986); Lorz *et al.*,

*Mol. Gen. Genet. 199*:178 (1985); Fromm *et al.*, *Nature 319*:791 (1986); Uchimiya *et al.*, *Mol.*

15    *Gen. Genet. 204*:204 (1986); Marcotte *et al.*, *Nature 335*:454-457 (1988), all of which are herein

incorporated by reference in their entirety).

Application of these systems to different plant strains depends upon the ability to

regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration

of cereals from protoplasts are described (Fujimura *et al.*, *Plant Tissue Culture Letters 2*:74

20    (1985); Toriyama *et al.*, *Theor Appl. Genet. 205*:34 (1986); Yamada *et al.*, *Plant Cell Rep. 4*:85

(1986); Abdullah *et al.*, *Biotechnolog. 4*:1087 (1986), all of which are herein incorporated by

reference in their entirety).

To transform plant strains that cannot be successfully regenerated from protoplasts, other

ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of

25    cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology*

*6*:397 (1988), the entirety of which is herein incorporated by reference). In addition, "particle

gun" or high-velocity microprojectile technology can be utilized (Vasil *et al., Bio/Technology* *10:*667 (1992), the entirety of which is herein incorporated by reference).

Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al., Nature 328:*70 (1987); Klein *et al., Proc. Natl. Acad. Sci. (U.S.A.) 85:*8502-8505 (1988); McCabe *et al., Bio/Technology 6:923* (1988), all of which are herein incorporated by reference in their entirety). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

Other methods of cell transformation can also be used and include but are not limited to introduction of DNA into plants by direct DNA transfer into pollen (Hess *et al., Intern Rev. Cytol. 107:*367 (1987); Luo *et al., Plant Mol Biol. Reporter 6:*165 (1988), all of which are herein incorporated by reference in their entirety), by direct injection of DNA into reproductive organs of a plant (Pena *et al., Nature 325:*274 (1987), the entirety of which is herein incorporated by reference), or by direct injection of DNA into the cells of immature embryos followed by the rehydration of desiccated embryos (Neuhaus *et al., Theor. Appl. Genet. 75:*30 (1987), the entirety of which is herein incorporated by reference).

The regeneration, development and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, In: *Methods for Plant Molecular Biology*, Academic Press, San Diego, CA, (1988), the entirety of which is herein incorporated by reference). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants. Otherwise, pollen obtained from the

regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

5        There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens* and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863; U.S.

10      Patent No. 5,159,135; U.S. Patent No. 5,518,908, all of which are herein incorporated by reference in their entirety); soybean (U.S. Patent No. 5,569,834; U.S. Patent No. 5,416,011; McCabe *et al., Biotechnology 6*:923 (1988); Christou *et al., Plant Physiol. 87*:671-674 (1988); all of which are herein incorporated by reference in their entirety); *Brassica* (U.S. Patent No. 5,463,174, the entirety of which is herein incorporated by reference); peanut (Cheng *et al., Plant*

15      *Cell Rep. 15*:653-657 (1996), McKently *et al., Plant Cell Rep. 14*:699-703 (1995), all of which are herein incorporated by reference in their entirety); papaya; and pea (Grant *et al., Plant Cell Rep. 15*:254-258 (1995), the entirety of which is herein incorporated by reference).

Transformation of monocotyledons using electroporation, particle bombardment and *Agrobacterium* have also been reported. Transformation and plant regeneration have been

20      achieved in asparagus (Bytebier *et al., Proc. Natl. Acad. Sci. (USA) 84*:5354 (1987), the entirety of which is herein incorporated by reference); barley (Wan and Lemaux, *Plant Physiol 104*:37 (1994), the entirety of which is herein incorporated by reference); maize (Rhodes *et al., Science 240*:204 (1988); Gordon-Kamm *et al., Plant Cell 2*:603-618 (1990); Fromm *et al., Bio/Technology 8*:833 (1990); Koziel *et al., Bio/Technology 11*:194 (1993); Armstrong *et al.,*

25      *Crop Science 35*:550-557 (1995); all of which are herein incorporated by reference in their entirety); oat (Somers *et al., Bio/Technology 10*:1589 (1992), the entirety of which is herein incorporated by reference); orchard grass (Horn *et al., Plant Cell Rep. 7*:469 (1988), the entirety

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of which is herein incorporated by reference); rice (Toriyama *et al., Theor Appl. Genet.* 205:34 (1986); Part *et al., Plant Mol. Biol.* 32:1135-1148 (1996); Abedinia *et al., Aust. J. Plant Physiol.* 24:133-141 (1997); Zhang and Wu, *Theor. Appl. Genet.* 76:835 (1988); Zhang *et al., Plant Cell Rep.* 7:379 (1988); Battraw and Hall, *Plant Sci.* 86:191-202 (1992); Christou *et al.,*

5      *Bio/Technology* 9:957 (1991), all of which are herein incorporated by reference in their entirety); rye (De la Pena *et al., Nature* 325:274 (1987), the entirety of which is herein incorporated by reference); sugarcane (Bower and Birch, *Plant J.* 2:409 (1992), the entirety of which is herein incorporated by reference); tall fescue (Wang *et al., Bio/Technology* 10:691 (1992), the entirety of which is herein incorporated by reference) and wheat (Vasil *et al., Bio/Technology* 10:667

10     (1992), the entirety of which is herein incorporated by reference; U.S. Patent No. 5,631,152, the entirety of which is herein incorporated by reference.)

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte *et al., Nature*

15     335:454-457 (1988), the entirety of which is herein incorporated by reference; Marcotte *et al., Plant Cell* 1:523-532 (1989), the entirety of which is herein incorporated by reference; McCarty *et al., Cell* 66:895-905 (1991), the entirety of which is herein incorporated by reference; Hattori *et al., Genes Dev.* 6:609-618 (1992), the entirety of which is herein incorporated by reference; Goff *et al., EMBO J.* 9:2517-2522 (1990), the entirety of which is herein incorporated by

20     reference). Transient expression systems may be used to functionally dissect gene constructs (*see generally*, Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995)).

Any of the nucleic acid molecules of the invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters, enhancers, etc. Further, any of the nucleic acid molecules of the invention may be

25     introduced into a plant cell in a manner that allows for overexpression of the protein or fragment thereof encoded by the nucleic acid molecule.

Cosuppression is the reduction in expression levels, usually at the level of RNA, of a particular endogenous gene or gene family by the expression of a homologous sense construct that is capable of transcribing mRNA of the same strandedness as the transcript of the endogenous gene (Napoli *et al.*, *Plant Cell* 2:279-289 (1990), the entirety of which is herein incorporated by reference; van der Krol *et al.*, *Plant Cell* 2:291-299 (1990), the entirety of which is herein incorporated by reference). Cosuppression may result from stable transformation with a single copy nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Prolls and Meyer, *Plant J.* 2:465-475 (1992), the entirety of which is herein incorporated by reference) or with multiple copies of a nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Mittlesten *et al.*, *Mol. Gen. Genet.* 244:325-330 (1994), the entirety of which is herein incorporated by reference). Genes, even though different, linked to homologous promoters may result in the cosuppression of the linked genes (Vaucheret, *C.R. Acad. Sci. III* 316:1471-1483 (1993), the entirety of which is herein incorporated by reference).

This technique has, for example, been applied to generate white flowers from red petunia and tomatoes that do not ripen on the vine. Up to 50% of petunia transformants that contained a sense copy of the glucoamylase (CHS) gene produced white flowers or floral sectors; this was as a result of the post-transcriptional loss of mRNA encoding CHS (Flavell, *Proc. Natl. Acad. Sci. (U.S.A.)* 91:3490-3496 (1994), the entirety of which is herein incorporated by reference); van Blokland *et al.*, *Plant J.* 6:861-877 (1994), the entirety of which is herein incorporated by reference). Cosuppression may require the coordinate transcription of the transgene and the endogenous gene and can be reset by a developmental control mechanism (Jorgensen, *Trends Biotechnol.* 8:340-344 (1990), the entirety of which is herein incorporated by reference; Meins and Kunz, In: *Gene Inactivation and Homologous Recombination in Plants*, Paszkowski (ed.), pp. 335-348, Kluwer Academic, Netherlands (1994), the entirety of which is herein incorporated by reference).

It is understood that one or more of the nucleic acids of the invention may be introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the cosuppression of an endogenous protein.

Antisense approaches are a way of preventing or reducing gene function by targeting the genetic material (Mol et al., FEBS Lett. 268:427-430 (1990), the entirety of which is herein incorporated by reference). The objective of the antisense approach is to use a sequence complementary to the target gene to block its expression and create a mutant cell line or organism in which the level of a single chosen protein is selectively reduced or abolished. Antisense techniques have several advantages over other 'reverse genetic' approaches. The site of inactivation and its developmental effect can be manipulated by the choice of promoter for antisense genes or by the timing of external application or microinjection. Antisense can manipulate its specificity by selecting either unique regions of the target gene or regions where it shares homology to other related genes (Hiatt et al., In: Genetic Engineering, Setlow (ed.), Vol. 11, New York: Plenum 49-63 (1989), the entirety of which is herein incorporated by reference).

The principle of regulation by antisense RNA is that RNA that is complementary to the target mRNA is introduced into cells, resulting in specific RNA:RNA duplexes being formed by base pairing between the antisense substrate and the target mRNA (Green et al., Annu. Rev. Biochem. 55:569-597 (1986), the entirety of which is herein incorporated by reference). Under one embodiment, the process involves the introduction and expression of an antisense gene sequence. Such a sequence is one in which part or all of the normal gene sequences are placed under a promoter in inverted orientation so that the 'wrong' or complementary strand is transcribed into a noncoding antisense RNA that hybridizes with the target mRNA and interferes with its expression (Takayama and Inouye, Crit. Rev. Biochem. Mol. Biol. 25:155-184 (1990), the entirety of which is herein incorporated by reference). An antisense vector is constructed by standard procedures and introduced into cells by transformation, transfection, electroporation, microinjection, infection, etc. The type of transformation and choice of vector will determine

whether expression is transient or stable. The promoter used for the antisense gene may influence the level, timing, tissue, specificity, or inducibility of the antisense inhibition.

It is understood that the activity of a protein in a plant cell may be reduced or depressed by growing a transformed plant cell containing a nucleic acid molecule of the present invnetion whose non-transcribed strand encodes a protein or fragment thereof.

Antibodies have been expressed in plants (Hiatt et al., Nature 342:76-78 (1989), the entirety of which is herein incorporated by reference; Conrad and Fielder, Plant Mol. Biol. 26:1023-1030 (1994), the entirety of which is herein incorporated by reference). Cytoplasmic expression of a scFv (single-chain Fv antibodies) has been reported to delay infection by artichoke mottled crinkle virus. Transgenic plants that express antibodies directed against endogenous proteins may exhibit a physiological effect (Philips et al., EMBO J. 16:4489-4496 (1997), the entirety of which is herein incorporated by reference; Marion-Poll, Trends in Plant Science 2:447-448 (1997), the entirety of which is herein incorporated by reference). For example, expressed anti-abscissic antibodies have been reported to result in a general perturbation of seed development (Philips et al., EMBO J. 16: 4489-4496 (1997)).

Antibodies that are catalytic may also be expressed in plants (abzymes). The principle behind abzymes is that since antibodies may be raised against many molecules, this recognition ability can be directed toward generating antibodies that bind transition states to force a chemical reaction forward (Persidas, Nature Biotechnology 15:1313-1315 (1997), the entirety of which is herein incorporated by reference; Baca et al., Ann. Rev. Biophys. Biomol. Struct. 26:461-493 (1997), the entirety of which is herein incorporated by reference). The catalytic abilities of abzymes may be enhanced by site directed mutagenesis. Examples of abzymes are, for example, set forth in U.S. Patent No: 5,658,753; U.S. Patent No. 5,632,990; U.S. Patent No. 5,631,137; U.S. Patent 5,602,015; U.S. Patent No. 5,559,538; U.S. Patent No. 5,576,174; U.S. Patent No. 5,500,358; U.S. Patent 5,318,897; U.S. Patent No. 5,298,409; U.S. Patent No. 5,258,289 and U.S. Patent No. 5,194,585, all of which are herein incorporated in their entirety.

It is understood that any of the antibodies of the invention may be expressed in plants and that such expression can result in a physiological effect. It is also understood that any of the expressed antibodies may be catalytic.

**(d) Antibodies**

One aspect of the invention concerns antibodies, single-chain antigen binding molecules, or other proteins that specifically bind to one or more of the protein or peptide molecules of the invention and their homologues, fusions or fragments. In a preferred embodiment, an antibody of the present invention binds to an amino acid selected from the group consisting of SEQ ID NO: 622 through 625. Such antibodies may be used to quantitatively or qualitatively detect the protein or peptide molecules of the invention. As used herein, an antibody or peptide is said to "specifically bind" to a protein or peptide molecule of the invention if such binding is not competitively inhibited by the presence of non-related molecules.

Nucleic acid molecules that encode all or part of the protein of the invention can be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may be a "fusion" molecule (*i.e.*, a part of a larger nucleic acid molecule) such that, upon expression, a fusion protein is produced. It is understood that any of the nucleic acid molecules of the invention may be expressed, via recombinant means, to yield proteins or peptides encoded by these nucleic acid molecules.

The antibodies that specifically bind proteins and protein fragments of the invention may be polyclonal or monoclonal and may comprise intact immunoglobulins, or antigen binding portions of immunoglobulins fragments (such as (F(ab'), F(ab')2), or single-chain immunoglobulins producible, for example, via recombinant means. It is understood that practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of antibodies (*see*, for example,

Harlow and Lane, In: *Antibodies: A Laboratory Manual,* Cold Spring Harbor Press, Cold Spring

Harbor, New York (1988), the entirety of which is herein incorporated by reference).

Murine monoclonal antibodies are particularly preferred. BALB/c mice are preferred for

this purpose, however, equivalent strains may also be used. The animals are preferably

5      immunized with approximately 25 µg of purified protein (or fragment thereof) that has been

emulsified in a suitable adjuvant (such as TiterMax adjuvant (Vaxcel, Norcross, GA)).

Immunization is preferably conducted at two intramuscular sites, one intraperitoneal site and one

subcutaneous site at the base of the tail. An additional i.v. injection of approximately 25 µg of

antigen is preferably given in normal saline three weeks later. After approximately 11 days

10      following the second injection, the mice may be bled and the blood screened for the presence of

anti-protein or peptide antibodies. Preferably, a direct binding Enzyme-Linked Immunoassay

(ELISA) is employed for this purpose.

More preferably, the mouse having the highest antibody titer is given a third i.v. injection

of approximately 25 µg of the same protein or fragment. The splenic leukocytes from this animal

15      may be recovered 3 days later and then permitted to fuse, most preferably, using polyethylene

glycol, with cells of a suitable myeloma cell line (such as, for example, the P3X63Ag8.653

myeloma cell line). Hybridoma cells are selected by culturing the cells under "HAT"

(hypoxanthine-aminopterin-thymine) selection for about one week. The resulting clones may

then be screened for their capacity to produce monoclonal antibodies ("mAbs"), preferably by

20      direct ELISA.

In one embodiment, anti-protein or peptide monoclonal antibodies are isolated using a

fusion of a protein or peptide of the invention, or conjugate of a protein or peptide of the

invention, as immunogens. Thus, for example, a group of mice can be immunized using a fusion

protein emulsified in Freund's complete adjuvant (*e.g.,* approximately 50 µg of antigen per

25      immunization). At three week intervals, an identical amount of antigen is emulsified in Freund's

incomplete adjuvant and used to immunize the animals. Ten days following the third

immunization, serum samples are taken and evaluated for the presence of antibody. If antibody

titers are too low, a fourth booster can be employed.  Polysera capable of binding the protein or peptide can also be obtained using this method.

In a preferred procedure for obtaining monoclonal antibodies, the spleens of the above-described immunized mice are removed, disrupted and immune splenocytes are isolated over a

5    ficoll gradient.  The isolated splenocytes are fused, using polyethylene glycol with BALB/c-derived HGPRT (hypoxanthine guanine phosphoribosyl transferase) deficient P3x63xAg8.653 plasmacytoma cells.  The fused cells are plated into 96 well microtiter plates and screened for hybridoma fusion cells by their capacity to grow in culture medium supplemented with hypothanthine, aminopterin and thymidine for approximately 2-3 weeks.

10    Hybridoma cells that arise from such incubation are preferably screened for their capacity to produce an immunoglobulin that binds to a protein of interest.  An indirect ELISA may be used for this purpose.  In brief, the supernatants of hybridomas are incubated in microtiter wells that contain immobilized protein.  After washing, the titer of bound immunoglobulin can be determined using, for example, a goat anti-mouse antibody conjugated to horseradish peroxidase.

15    After additional washing, the amount of immobilized enzyme is determined (for example through the use of a chromogenic substrate).  Such screening is performed as quickly as possible after the identification of the hybridoma in order to ensure that a desired clone is not overgrown by non-secreting neighbor cells.  Desirably, the fusion plates are screened several times since the rates of hybridoma growth vary.  In a preferred sub-embodiment, a different antigenic form may

20    be used to screen the hybridoma.  Thus, for example, the splenocytes may be immunized with one immunogen, but the resulting hybridomas can be screened using a different immunogen.  It is understood that any of the protein or peptide molecules of the invention may be used to raise antibodies.

As discussed below, such antibody molecules or their fragments may be used for

25    diagnostic purposes.  Where the antibodies are intended for diagnostic purposes, it may be desirable to derivatize them, for example with a ligand group (such as biotin) or a detectable marker group (such as a fluorescent group, a radioisotope or an enzyme).

The ability to produce antibodies that bind the protein or peptide molecules of the invention permits the identification of mimetic compounds derived from those molecules. These mimetic compounds may contain a fragment of the protein or peptide or merely a structurally similar region and nonetheless exhibits an ability to specifically bind to antibodies directed against that compound.

It is understood that any of the agents of the invention can be substantially purified and/or be biologically active and/or recombinant.

(e)     **Exemplary Uses**

Nucleic acid molecules and fragments thereof of the invention may be employed to obtain other nucleic acid molecules from the same species (nucleic acid molecules from maize may be utilized to obtain other nucleic acid molecules from maize). Such nucleic acid molecules include the nucleic acid molecules that encode the complete coding sequence of a protein and promoters and flanking sequences of such molecules. In addition, such nucleic acid molecules include nucleic acid molecules that encode for other isozymes or gene family members. Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries. Methods for forming such libraries are well known in the art.

Nucleic acid molecules and fragments thereof of the invention may also be employed to obtain nucleic acid homologs. Such homologs include the nucleic acid molecule of other plants or other organisms (*e.g.*, alfalfa, *Arabidopsis*, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus*, etc.) including the nucleic acid molecules that encode, in whole or in part, protein homologs of other plant species or other organisms, sequences of genetic elements, such as promoters and transcriptional regulatory elements. Particularly preferred plants are selected from the group

consisting of maize, canola, soybean, crambe, mustard, castor bean, peanut, sesame, cottonseed, linseed, safflower, oil palm, flax and sunflower.

Such molecules can be readily obtained by using the above-described nucleic acid molecules or fragments thereof to screen cDNA or genomic libraries obtained from such plant

5    species. Methods for forming such libraries are well known in the art. Such homolog molecules may differ in their nucleotide sequences from those found in one or more of SEQ ID NOs: 1-4, 6-29 or complements thereof because complete complementarity is not needed for stable hybridization. The nucleic acid molecules of the invention therefore also include molecules that, although capable of specifically hybridizing with the nucleic acid molecules may lack "complete

10   complementarity."

Any of a variety of methods may be used to obtain one or more of the above-described nucleic acid molecules (Zamechik *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 83*:4143-4146 (1986); Goodchild *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 85*:5507-5511 (1988); Wickstrom *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 85*:1028-1032 (1988); Holt *et al.*, *Molec. Cell. Biol. 8*:963-973 (1988);

15   Gerwirtz *et al.*, *Science 242*:1303-1306 (1988); Anfossi *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:3379-3383 (1989); Becker *et al.*, *EMBO J. 8*:3685-3691 (1989)). Automated nucleic acid synthesizers may be employed for this purpose. In lieu of such synthesis, the disclosed nucleic acid molecules may be used to define a pair of primers that can be used with the polymerase chain reaction (Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol. 51*:263-273 (1986); Erlich

20   *et al.*, European Patent 50,424; European Patent 84,796; European Patent 258,017; European Patent 237,362; Mullis, European Patent 201,184; Mullis *et al.*, U.S. Patent 4,683,202; Erlich, U.S. Patent 4,582,788; and Saiki *et al.*, U.S. Patent 4,683,194) to amplify and obtain any desired nucleic acid molecule or fragment.

Promoter sequences and other genetic elements, including but not limited to

25   transcriptional regulatory flanking sequences, associated with one or more of the disclosed nucleic acid sequences can also be obtained using the disclosed nucleic acid sequence provided herein. In one embodiment, such sequences are obtained by incubating nucleic acid molecules of

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the present invention with members of genomic libraries and recovering clones that hybridize to such nucleic acid molecules thereof. In a second embodiment, methods of "chromosome walking," or inverse PCR may be used to obtain such sequences (Frohman *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 85*:8998-9002 (1988); Ohara *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:5673-5677 (1989); Pang *et al.*, *Biotechniques 22*:1046-1048 (1977); Huang *et al.*, *Methods Mol. Biol. 69*:89-96 (1997); Huang *et al.*, *Method Mol. Biol. 67*:287-294 (1997); Benkel *et al.*, *Genet. Anal. 13*:123-127 (1996); Hartl *et al.*, *Methods Mol. Biol. 58*:293-301 (1996)). The term "chromosome walking" means a process of extending a genetic map by successive hybridization steps.

The nucleic acid molecules of the invention may be used to isolate promoters of cell enhanced, cell specific, tissue enhanced, tissue specific, developmentally or environmentally regulated expression profiles. Isolation and functional analysis of the 5' flanking promoter sequences of these genes from genomic libraries, for example, using genomic screening methods and PCR techniques would result in the isolation of useful promoters and transcriptional regulatory elements. These methods are known to those of skill in the art and have been described (See, for example, Birren *et al.*, *Genome Analysis: Analyzing DNA*, 1, (1997), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.). Promoters obtained utilizing the nucleic acid molecules of the invention could also be modified to affect their control characteristics. Examples of such modifications would include but are not limited to enhancer sequences. Such genetic elements could be used to enhance gene expression of new and existing traits for crop improvement.

Another subset of the nucleic acid molecules of the invention includes nucleic acid molecules that are markers. The markers can be used in a number of conventional ways in the field of molecular genetics. Such markers include nucleic acid molecules SEQ ID NOs: 1-4, 6-29 or complements thereof or fragments of either that can act as markers and other nucleic acid molecules of the present invention that can act as markers.

Genetic markers of the invention include "dominant" or "codominant" markers. "Codominant markers" reveal the presence of two or more alleles (two per diploid individual) at

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a locus. "Dominant markers" reveal the presence of only a single allele per locus. The presence of the dominant marker phenotype (e.g., a band of DNA) is an indication that one allele is in either the homozygous or heterozygous condition. The absence of the dominant marker phenotype (*e.g.*, absence of a DNA band) is merely evidence that "some other" undefined allele

5    is present. In the case of populations where individuals are predominantly homozygous and loci are predominately dimorphic, dominant and codominant markers can be equally valuable. As populations become more heterozygous and multi-allelic, codominant markers often become more informative of the genotype than dominant markers. Marker molecules can be, for example, capable of detecting polymorphisms such as single nucleotide polymorphisms (SNPs).

10    The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem. 55*:831-854 (1986)). A "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species. The variant sequence and the "original" sequence co-exist in the species' population. In some instances, such co-existence is in stable or

15    quasi-stable equilibrium.

A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the original sequence (i.e., the original "allele") whereas other members may have the variant sequence (i.e., the variant "allele"). In the simplest case, only one variant sequence may exist and the polymorphism is thus said to be di-

20    allelic. In other cases, the species' population may contain multiple alleles and the polymorphism is termed tri-allelic, etc. A single gene may have multiple different unrelated polymorphisms. For example, it may have a di-allelic polymorphism at one site and a multi-allelic polymorphism at another site.

The variation that defines the polymorphism may range from a single nucleotide variation

25    to the insertion or deletion of extended regions within a gene. In some cases, the DNA sequence variations are in regions of the genome that are characterized by short tandem repeats (STRs) that include tandem di- or tri-nucleotide repeated motifs of nucleotides. Polymorphisms

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characterized by such tandem repeats are referred to as "variable number tandem repeat" ("VNTR") polymorphisms. VNTRs have been used in identity analysis (Weber, U.S. Patent 5,075,217; Armour *et al., FEBS Lett. 307*:113-115 (1992); Jones *et al., Eur. J. Haematol. 39*:144-147 (1987); Horn *et al.*, PCT Patent Application WO91/14003; Jeffreys, European Patent Application 370,719; Jeffreys, U.S. Patent 5,175,082; Jeffreys *et al., Amer. J. Hum. Genet. 39*:11-24 (1986); Jeffreys *et al., Nature 316*:76-79 (1985); Gray *et al., Proc. R. Acad. Soc. Lond. 243*:241-253 (1991); Moore *et al., Genomics 10*:654-660 (1991); Jeffreys *et al., Anim. Genet. 18*:1-15 (1987); Hillel *et al., Anim. Genet. 20*:145-155 (1989); Hillel *et al., Genet. 124*:783-789 (1990)).

The detection of polymorphic sites in a sample of DNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

In an alternative embodiment, such polymorphisms can be detected through the use of a marker nucleic acid molecule that is physically linked to such polymorphism(s). For this purpose, marker nucleic acid molecules comprising a nucleotide sequence of a polynucleotide located within 1 mb of the polymorphism(s) and more preferably within 100kb of the polymorphism(s) and most preferably within 10kb of the polymorphism(s) can be employed.

The identification of a polymorphism can be determined in a variety of ways. By correlating the presence or absence of it in a plant with the presence or absence of a phenotype, it is possible to predict the phenotype of that plant. If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (e.g., a VNTR polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, organisms that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length

polymorphisms" ("RFLPs") (Glassberg, UK Patent Application 2135774; Skolnick *et al.*, *Cytogen. Cell Genet.* *32*:58-67 (1982); Botstein *et al.*, *Ann. J. Hum. Genet.* *32*:314-331 (1980); Fischer *et al.*, (PCT Application WO90/13668; Uhlen, PCT Application WO90/11369).

Polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) analysis (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996)); Orita *et al.*, *Genomics 5*:874-879 (1989)). A number of protocols have been described for SSCP including, but not limited to, Lee *et al.*, *Anal. Biochem.* *205*:289-293 (1992); Suzuki *et al.*, *Anal. Biochem.* *192*:82-84 (1991); Lo *et al.*, *Nucleic Acids Research 20*:1005-1009 (1992); Sarkar *et al.*, *Genomics 13*:441-443 (1992). It is understood that one or more of the nucleic acids of the invention, may be utilized as markers or probes to detect polymorphisms by SSCP analysis.

Polymorphisms may also be found using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA (Vos *et al.*, *Nucleic Acids Res. 23*:4407-4414 (1995)). This method allows for the specific co-amplification of high numbers of restriction fragments, which can be visualized by PCR without knowledge of the nucleic acid sequence. It is understood that one or more of the nucleic acids of the invention may be utilized as markers or probes to detect polymorphisms by AFLP analysis or for fingerprinting RNA.

Polymorphisms may also be found using random amplified polymorphic DNA (RAPD) (Williams *et al.*, *Nucl. Acids Res. 18*:6531-6535 (1990)) and cleaveable amplified polymorphic sequences (CAPS) (Lyamichev *et al.*, *Science 260*:778-783 (1993)). It is understood that one or more of the nucleic acid molecules of the invention, may be utilized as markers or probes to detect polymorphisms by RAPD or CAPS analysis.

Single Nucleotide Polymorphisms (SNPs) generally occur at greater frequency than other polymorphic markers and are spaced with a greater uniformity throughout a genome than other reported forms of polymorphism. The greater frequency and uniformity of SNPs means that

there is greater probability that such a polymorphism will be found near or in a genetic locus of

interest than would be the case for other polymorphisms. SNPs are located in protein-coding

regions and noncoding regions of a genome. Some of these SNPs may result in defective or

variant protein expression (*e.g.*, as a result of mutations or defective splicing). Analysis

5      (genotyping) of characterized SNPs can require only a plus/minus assay rather than a lengthy

measurement, permitting easier automation.

SNPs can be characterized using any of a variety of methods. Such methods include the

direct or indirect sequencing of the site, the use of restriction enzymes (Botstein *et al.*, *Am. J.*

*Hum. Genet. 32*:314-331 (1980), the entirety of which is herein incorporated reference;

10     Konieczny and Ausubel, *Plant J. 4*:403-410 (1993), the entirety of which is herein incorporated

by reference), enzymatic and chemical mismatch assays (Myers *et al.*, *Nature 313*:495-498

(1985), the entirety of which is herein incorporated by reference), allele-specific PCR (Newton *et*

*al.*, *Nucl. Acids Res. 17*:2503-2516 (1989), the entirety of which is herein incorporated by

reference; Wu *et al.*, *Proc. Natl. Acad. Sci. USA 86*:2757-2760 (1989), the entirety of which is

15     herein incorporated by reference), ligase chain reaction (Barany, *Proc. Natl. Acad. Sci. USA*

*88*:189-193 (1991), the entirety of which is herein incorporated by reference), single-strand

conformation polymorphism analysis (Labrune *et al.*, *Am. J. Hum. Genet. 48*: 1115-1120 (1991),

the entirety of which is herein incorporated by reference), single base primer extension

(Kuppuswamy *et al.*, *Proc. Natl. Acad. Sci. USA 88*:1143-1147 (1991), Goelet US 6,004,744;

20     Goelet 5,888,819; all of which are herein incorporated by reference in their entirety ), solid-phase

ELISA-based oligonucleotide ligation assays (Nikiforov *et al.*, *Nucl. Acids Res. 22*:4167-4175

(1994), dideoxy fingerprinting (Sarkar *et al.*, *Genomics 13*:441-443 (1992), the entirety of which

is herein incorporated by reference), oligonucleotide fluorescence-quenching assays (Livak *et al.*,

*PCR Methods Appl. 4*:357-362 (1995a), the entirety of which is herein incorporated by

25     reference), 5'-nuclease allele-specific hybridization TaqMan™ assay (Livak *et al.*, *Nature Genet.*

*9*:341-342 (1995), the entirety of which is herein incorporated by reference), template-directed

dye-terminator incorporation (TDI) assay (Chen and Kwok, *Nucl. Acids Res. 25*:347-353 (1997),

the entirety of which is herein incorporated by reference), allele-specific molecular beacon assay

(Tyagi *et al.*, *Nature Biotech. 16*: 49-53 (1998), the entirety of which is herein incorporated by

reference), PinPoint assay ( Haff and Smirnov, *Genome Res. 7*: 378-388 (1997), the entirety of

which is herein incorporated by reference), dCAPS analysis (Neff *et al.*, *Plant J. 14*:387-392

5    (1998), the entirety of which is herein incorporated by reference), pyrosequencing (Ronaghi *et al*,

*Analytical Biochemistry 267*:65-71 (1999); Ronaghi *et al* PCT application WO 98/13523; Nyren

*et al* PCT application WO 98/28440, all of which are herein incorporated by reference in their

entirety; http//www.pyrosequencing.com), using mass spectrometry, *e.g.* the Masscode ™ system

(Howbert *et al* WO 99/05319; Howber *et al* WO 97/27331, all of which are herein incorporated

10    by reference in their entirety; http//www.rapigene.com; Becker *et al* PCT application WO

98/26095; Becker *et al* PCT application; WO 98/12355; Becker *et al* PCT application WO

97/33000; Monforte *et al* US 5,965,363, all of which are herein incorporated by reference in

their entirety), invasive cleavage of oligonucleotide probes (Lyamichev *et al Nature*

*Biotechnology 17*:292-296, herein incorporated by reference in its entirety; http//www.twt.com),

15    and using high density oligonucleotide arrays (Hacia *et al Nature Genetics 22*:164-167; herein

incorporated by reference in its entirety; http//www.affymetrix.com).

Polymorphisms may also be detected using allele-specific oligonucleotides (ASO),

which, can be for example, used in combination with hybridization based technology including

southern, northern, and dot blot hybridizations, reverse dot blot hybridizations and hybridizations

20    performed on microarray and related technology.

The stringency of hybridization for polymorphism detection is highly dependent upon a

variety of factors, including length of the allele-specific oligonucleotide, sequence composition,

degree of complementarity (*i.e.* presence or absence of base mismatches), concentration of salts

and other factors such as formamide, and temperature. These factors are important both during

25    the hybridization itself and during subsequent washes performed to remove target polynucleotide

that is not specifically hybridized. In practice, the conditions of the final, most stringent wash are

most critical. In addition, the amount of target polynucleotide that is able to hybridize to the

allele-specific oligonucleotide is also governed by such factors as the concentration of both the ASO and the target polynucleotide, the presence and concentration of factors that act to "tie up" water molecules, so as to effectively concentrate the reagents (*e.g.*, PEG, dextran, dextran sulfate, *etc.*), whether the nucleic acids are immobilized or in solution, and the duration of hybridization and washing steps.

Hybridizations are preferably performed below the melting temperature ($T_m$) of the ASO. The closer the hybridization and/or washing step is to the $T_m$, the higher the stringency. $T_m$ for an oligonucleotide may be approximated, for example, according to the following formula: $T_m = 81.5 + 16.6 \times (log10[Na+]) + 0.41 \times (\%G+C) - 675/n$; where [Na+] is the molar salt concentration of Na+ or any other suitable cation and n = number of bases in the oligonucleotide. Other formulas for approximating $T_m$ are available and are known to those of ordinary skill in the art.

Stringency is preferably adjusted so as to allow a given ASO to differentially hybridize to a target polynucleotide of the correct allele and a target polynucleotide of the incorrect allele. Preferably, there will be at least a two-fold differential between the signal produced by the ASO hybridizing to a target polynucleotide of the correct allele and the level of the signal produced by the ASO cross-hybridizing to a target polynucleotide of the incorrect allele (*e.g.*, an ASO specific for a mutant allele cross-hybridizing to a wild-type allele). In more preferred embodiments of the present invention, there is at least a five-fold signal differential. In highly preferred embodiments of the present invention, there is at least an order of magnitude signal differential between the ASO hybridizing to a target polynucleotide of the correct allele and the level of the signal produced by the ASO cross-hybridizing to a target polynucleotide of the incorrect allele.

While certain methods for detecting polymorphisms are described herein, other detection methodologies may be utilized. For example, additional methodologies are known and set forth, in Birren *et al.*, *Genome Analysis*, 4:135-186, *A Laboratory Manual. Mapping Genomes*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1999); Maliga *et al.*, *Methods in Plant Molecular Biology. A Laboratory Course Manual*, Cold Spring Harbor Laboratory Press, Cold

Spring Harbor, NY (1995); Paterson, *Biotechnology Intelligence Unit: Genome Mapping in Plants*, R.G. Landes Co., Georgetown, TX, and Academic Press, San Diego, CA (1996); *The Maize Handbook*, Freeling and Walbot, eds., Springer-Verlag, New York, NY (1994); *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Elles, ed., Humana Press,

5      Totowa, NJ (1996); Clark, ed., *Plant Molecular Biology: A Laboratory Manual*, Clark, ed., Springer-Verlag, Berlin, Germany (1997), all of which are herein incorporated by reference in their entirety.

Requirements for marker-assisted selection in a plant breeding program are: (1) the marker(s) should co-segregate or be closely linked with the desired trait; (2) an efficient means of

10    screening large populations for the molecular marker(s) should be available; and (3) the screening technique should have high reproducibility across laboratories and preferably be economical to use and be user-friendly.

The genetic linkage of marker molecules can be established by a gene mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics*

15    *121*:185-199 (1989) and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics 121*:185-199 (1989) and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL*, Whitehead Institute for Biomedical Research, Massachusetts, (1990). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and

20    Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY). Use of Qgene software is a particularly preferred approach.

A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an odds ratio (LOD) is then calculated as: LOD = $\log_{10}$ (MLE for the presence of a QTL/MLE given no linked

25    QTL).

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL than in its absence. The LOD threshold value for avoiding a

false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein, *Genetics 121*:185-199 (1989) and further described by Arús and Moreno-González , *Plant Breeding*, Hayward *et al.*, (eds.) Chapman & Hall, London, pp. 314-331 (1993).

5          In a preferred embodiment of the present invention the nucleic acid marker exhibits a LOD score of greater than 2.0, more preferably 2.5, even more preferably greater than 3.0 or 4.0 with the trait or phenotype of interest. In a preferred embodiment, the trait of interest is altered, preferably increased phytosterol levels or compositions.

           Additional models can be used. Many modifications and alternative approaches to
10    interval mapping have been reported, including the use non-parametric methods (Kruglyak and Lander, *Genetics 139:*1421-1428 (1995)). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breeding*, van Oijen and Jansen (eds.), Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke,
15    *Advances in Plant Breeding*, Blackwell, Berlin, 16 (1994)). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics 136*:1447-1455 (1994), and Zeng, *Genetics 136*:1457-1468 (1994) . Generally, the use of cofactors reduces the bias and sampling error of
20    the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding*, van Oijen and Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics 136*:1457-1468 (1994), herein incorporated by reference in its entirety). These models can be extended to multi-environment experiments to analyze genotype-
25    environment interactions (Jansen *et al.*, *Theo. Appl. Genet. 91:*33-37 (1995), herein incorporated by reference in its entirety).

It is understood that one or more of the nucleic acid molecules of the invention may be used as molecular markers. It is also understood that one or more of the protein molecules of the invention may be used as molecular markers.

In a preferred embodiment, the polymorphism is present and screened for in a mapping population, e.g. a collection of plants capable of being used with markers such as polymorphic markers to map genetic position of traits. The choice of appropriate mapping population often depends on the type of marker systems employed (Tanksley et al., J.P. Gustafson and R. Appels (eds.). Plenum Press, New York, pp. 157-173 (1988), the entirety of which is herein incorporated by reference). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted x exotic) and generally yield greatly reduced linkage distances. Wide crosses will usually provide segregating populations with a relatively large number of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

An $F_2$ population is the first generation of selfing (self-pollinating) after the hybrid seed is produced. Usually a single $F_1$ plant is selfed to generate a population segregating for all the genes in Mendelian (1:2:1) pattern. Maximum genetic information is obtained from a completely classified $F_2$ population using a codominant marker system (Mather, Measurement of Linkage in Heredity: Methuen and Co., (1938), the entirety of which is herein incorporated by reference). In the case of dominant markers, progeny tests (e.g., $F_3$, $BCF_2$) are required to identify the heterozygotes, in order to classify the population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of $F_2$ individuals is often used in map construction where phenotypes do not consistently reflect genotype (e.g. disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations e.g. $F_3$ or $BCF_2$) can be used in map construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations ($F_2$, $F_3$), where linkage groups have not been completely disassociated by recombination events (i.e., maximum disequilibrium).

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Recombinant inbred lines (RIL) (genetically related lines; usually >F5, developed from

continuously selfing F2 lines towards homozygosity) can be used as a mapping population.

Information obtained from dominant markers can be maximized by using RIL because all loci are

homozygous or nearly so.  Under conditions of tight linkage (*i.e.*, about <10% recombination),

5      dominant and co-dominant markers evaluated in RIL populations provide more information per

individual than either marker type in backcross populations (Reiter. *Proc. Natl. Acad. Sci.*

*(U.S.A.)* *89*:1477-1481 (1992), the entirety of which is herein incorporated by reference).

However, as the distance between markers becomes larger (*i.e.*, loci become more independent),

the information in RIL populations decreases dramatically when compared to codominant

10     markers.

Backcross populations (*e.g.*, generated from a cross between a successful variety

(recurrent parent) and another variety (donor parent) carrying a trait not present in the former)

can be utilized as a mapping population.  A series of backcrosses to the recurrent parent can be

made to recover most of its desirable traits.  Thus a population is created consisting of individuals

15     nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic

regions from the donor parent.  Backcross populations can be useful for mapping dominant

markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent

have contrasting polymorphic marker alleles (Reiter *et al., Proc. Natl. Acad. Sci. (U.S.A.)*

*89*:1477-1481 (1992), the entirety of which is herein incorporated by reference).  Information

20     obtained from backcross populations using either codominant or dominant markers is less than

that obtained from F2 populations because one, rather than two, recombinant gamete is sampled

per plant.  Backcross populations, however, are more informative (at low marker saturation)

when compared to RILs as the distance between linked loci increases in RIL populations (*i.e.*

about .15% recombination).  Increased recombination can be beneficial for resolution of tight

25     linkages, but may be undesirable in the construction of maps with low marker saturation.

Near-isogenic lines (NIL) (created by many backcrosses to produce a collection of

individuals that is nearly identical in genetic composition except for the trait or genomic region

under interrogation) can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci is expected to map to a selected region.

Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* 88:9828-9832 (1991), the entirety of which is herein incorporated by reference). In BSA, two bulked DNA samples are drawn from a segregating population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but arbitrary at unlinked regions (*i.e.* heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

In an aspect of the present invention, one or more of the nucleic molecules of the present invention are used to determine the level (*i.e.*, the concentration of mRNA in a sample, *etc.*) in a plant (preferably maize, canola, soybean, crambe, mustard, castor bean, peanut, sesame, cottonseed, linseed, safflower, oil palm, flax or sunflower) or pattern (*i.e.*, the kinetics of expression, rate of decomposition, stability profile, *etc.*) of the expression of a protein encoded in part or whole by one or more of the nucleic acid molecule of the present invention (collectively, the "Expression Response" of a cell or tissue).

As used herein, the Expression Response manifested by a cell or tissue is said to be "altered" if it differs from the Expression Response of cells or tissues of plants not exhibiting the phenotype. To determine whether a Expression Response is altered, the Expression Response manifested by the cell or tissue of the plant exhibiting the phenotype is compared with that of a similar cell or tissue sample of a plant not exhibiting the phenotype. As will be appreciated, it is not necessary to re-determine the Expression Response of the cell or tissue sample of plants not exhibiting the phenotype each time such a comparison is made; rather, the Expression Response of a particular plant may be compared with previously obtained values of normal plants. As used herein, the phenotype of the organism is any of one or more characteristics of an organism (*e.g.* disease resistance, pest tolerance, environmental tolerance such as tolerance to abiotic stress,

male sterility, quality improvement or yield *etc.*). A change in genotype or phenotype may be transient or permanent. Also as used herein, a tissue sample is any sample that comprises more than one cell. In a preferred aspect, a tissue sample comprises cells that share a common characteristic (e.g. derived from root, seed, flower, leaf, stem or pollen etc.).

5          In one aspect of the present invention, an evaluation can be conducted to determine whether a particular mRNA molecule is present. One or more of the nucleic acid molecules of the present invention are utilized to detect the presence or quantity of the mRNA species. Such molecules are then incubated with cell or tissue extracts of a plant under conditions sufficient to permit nucleic acid hybridization. The detection of double-stranded probe-mRNA hybrid

10        molecules is indicative of the presence of the mRNA; the amount of such hybrid formed is proportional to the amount of mRNA. Thus, such probes may be used to ascertain the level and extent of the mRNA production in a plant's cells or tissues. Such nucleic acid hybridization may be conducted under quantitative conditions (thereby providing a numerical value of the amount of the mRNA present). Alternatively, the assay may be conducted as a qualitative assay that

15        indicates either that the mRNA is present, or that its level exceeds a user set, predefined value.

A number of methods can be used to compare the expression response between two or more samples of cells or tissue. These methods include hybridization assays, such as northerns, RNAse protection assays, and *in situ* hybridization. Alternatively, the methods include PCR-type assays. In a preferred method, the expression response is compared by hybridizing nucleic acids

20        from the two or more samples to an array of nucleic acids. The array contains a plurality of suspected sequences known or suspected of being present in the cells or tissue of the samples.

An advantage of *in situ* hybridization over more conventional techniques for the detection of nucleic acids is that it allows an investigator to determine the precise spatial population (Angerer *et al., Dev. Biol. 101*:477-484 (1984); Angerer *et al., Dev. Biol. 112*:157-166 (1985);

25        Dixon *et al., EMBO J. 10*:1317-1324 (1991)). *In situ* hybridization may be used to measure the steady-state level of RNA accumulation (Hardin *et al., J. Mol. Biol. 202*:417-431 (1989)). A number of protocols have been devised for *in situ* hybridization, each with tissue preparation,

hybridization and washing conditions (Meyerowitz, *Plant Mol. Biol. Rep.* 5:242-250 (1987); Cox

and Goldberg, In: *Plant Molecular Biology: A Practical Approach,* Shaw (ed.), pp. 1-35, IRL

Press, Oxford (1988); Raikhel *et al., In situ RNA hybridization in plant tissues,* In: *Plant*

*Molecular Biology Manual,* vol. B9:1-32, Kluwer Academic Publisher, Dordrecht, Belgium

5      (1989)).

In situ hybridization also allows for the localization of proteins within a tissue or cell

(Wilkinson, *In Situ Hybridization,* Oxford University Press, Oxford (1992); Langdale, *In Situ*

*Hybridization* In: *The Maize Handbook,* Freeling and Walbot (eds.), pp. 165-179, Springer-

Verlag, New York (1994)). It is understood that one or more of the molecules of the invention,

10     preferably one or more of the nucleic acid molecules or fragments thereof of the invention or one

or more of the antibodies of the invention may be utilized to detect the level or pattern of a

protein or mRNA thereof by *in situ* hybridization.

Fluorescent *in situ* hybridization allows the localization of a particular DNA sequence

along a chromosome, which is useful, among other uses, for gene mapping, following

15     chromosomes in hybrid lines, or detecting chromosomes with translocations, transversions or

deletions. *In situ* hybridization has been used to identify chromosomes in several plant species

(Griffor *et al., Plant Mol. Biol.* 17:101-109 (1991); Gustafson *et al., Proc. Natl. Acad. Sci.*

*(U.S.A.)* 87:1899-1902 (1990); Mukai and Gill, *Genome* 34:448-452 (1991); Schwarzacher and

Heslop-Harrison, *Genome* 34:317-323 (1991); Wang *et al., Jpn. J. Genet.* 66:313-316 (1991);

20     Parra and Windle, *Nature Genetics* 5:17-21 (1993)). It is understood that the nucleic acid

molecules of the invention may be used as probes or markers to localize sequences along a

chromosome.

Another method to localize the expression of a molecule is tissue printing. Tissue

printing provides a way to screen, at the same time on the same membrane many tissue sections

25     from different plants or different developmental stages (Yomo and Taylor, *Planta* 112:35-43

(1973); Harris and Chrispeels, *Plant Physiol.* 56:292-299 (1975); Cassab and Varner, *J. Cell.*

*Biol.* 105:2581-2588 (1987); Spruce *et al., Phytochemistry* 26:2901-2903 (1987); Barres *et al.,*

*Neuron 5:*527-544 (1990); Reid and Pont-Lezica, *Tissue Printing: Tools for the Study of Anatomy, Histochemistry and Gene Expression,* Academic Press, New York, New York (1992); Reid *et al., Plant Physiol. 93:*160-165 (1990); Ye *et al., Plant J. 1:*175-183 (1991)).

A microarray-based method for high-throughput monitoring of gene expression may be

5    utilized to measure expression response. This 'chip'-based approach involves microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding mRNA (Schena *et al., Science 270:*467-470 (1995), the entirety of which is herein incorporated by reference; http://cmgm.stanford.edu/pbrown/array.html; Shalon, Ph.D. Thesis, Stanford University (1996), the entirety of which is herein incorporated by

10   reference). Hybridization to a microarray can be used to efficiently analyze the presence and/or amount of a number of nucleotide sequences simultaneously.

Several microarray methods have been described. One method compares the sequences to be analyzed by hybridization to a set of oligonucleotides representing all possible subsequences (Bains and Smith, *J. Theor. Biol. 135:*303-307 (1989), the entirety of which is

15   herein incorporated by reference). A second method hybridizes the sample to an array of oligonucleotide or cDNA molecules. An array consisting of oligonucleotides complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount, and detect single nucleotide differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be screened with protein molecules or

20   fragments thereof to determine nucleic acid molecules that specifically bind protein molecules or fragments thereof.

The microarray approach may be used with polypeptide targets (U.S. Patent No. 5,445,934; U.S. Patent No: 5,143,854; U.S. Patent No. 5,079,600; U.S. Patent No. 4,923,901, all of which are herein incorporated by reference in their entirety). Essentially, polypeptides are

25   synthesized on a substrate (microarray) and these polypeptides can be screened with either protein molecules or fragments thereof or nucleic acid molecules in order to screen for either protein molecules or fragments thereof or nucleic acid molecules that specifically bind the target

polypeptides. (Fodor *et al.*, *Science 251*:767-773 (1991), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules or protein or fragments thereof of the invention may be utilized in a microarray-based method.

In a preferred embodiment of the present invention microarrays may be prepared that

5    comprise nucleic acid molecules where preferably at least 10%, preferably at least 25%, more preferably at least 50% and even more preferably at least 75%, 80%, 85%, 90% or 95% of the nucleic acid molecules located on that array are selected from the group of nucleic acid molecules that specifically hybridize to one or more nucleic acid molecule having a nucleic acid sequence selected from the group of SEQ ID NO: 1 through SEQ ID NO: 621 or complements

10    thereof or fragments of either.

In another preferred embodiment of the present invention microarrays may be prepared that comprise nucleic acid molecules where preferably at least 10%, preferably at least 25%, more preferably at least 50% and even more preferably at least 75%, 80%, 85%, 90% or 95% of the nucleic acid molecules located on that array are selected from the group of nucleic acid

15    molecules having a nucleic acid sequence selected from the group of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragments of either.

In a preferred embodiment of the present invention microarrays may be prepared that comprise nucleic acid molecules where such nucleic acid molecules encode at least one, preferably at least two, more preferably at least three, even more preferably at least four, five or

20    six proteins or fragments thereof selected from the group consisting of HES1, HMGCoA reductase, squalene synthase, cycloartenol synthase, SMTII and UPC2. In even more preferred embodiment of the present invention microarrays may be prepared that comprise nucleic acid molecules where such nucleic acid molecules encode at least one, preferably at least two, more preferably at least three, even more preferably at least four, five or six proteins or fragments

25    thereof selected from the group consisting of a fungal, more preferably a yeast HES1, a plant, more preferably a maize, soybean or *Arabidopsis* HES1, a plant, more preferably a rubber or an *Arabidopsis* HMGCoA reductase, a plant, more preferably an *Arabidopsis* squalene synthase, a

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plant, more preferably an *Arabidopsis* cycloartenol synthase, a plant, more preferably an *Arabidopsis* SMTII and a fungus, more preferably an yeast UPC2.

Site directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a technique that allows one or more of the amino acids encoded by a nucleic acid

5    molecule to be altered (*e.g.*, a threonine to be replaced by a methionine). At least three basic methods for site directed mutagenesis can be employed. These are cassette mutagenesis (Wells *et al.*, *Gene 34*:315-323 (1985), the entirety of which is herein incorporated by reference), primer extension (Gilliam *et al.*, *Gene 12*:129-137 (1980), the entirety of which is herein incorporated by reference; Zoller and Smith, *Methods Enzymol. 100*:468-500 (1983), the entirety of which is

10    herein incorporated by reference; Dalbadie-McFarland *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* *79*:6409-6413 (1982), the entirety of which is herein incorporated by reference) and methods based upon PCR (Scharf *et al.*, *Science 233*:1076-1078 (1986), the entirety of which is herein incorporated by reference; Higuchi *et al.*, *Nucleic Acids Res. 16*:7351-7367 (1988), the entirety of which is herein incorporated by reference). Site directed mutagenesis approaches are also

15    described in U.S. Patent 5,811,238, European Patent 0 385 962, the entirety of which is herein incorporated by reference; European Patent 0 359 472, the entirety of which is herein incorporated by reference; and PCT Patent Application WO 93/07278, the entirety of which is herein incorporated by reference.

Site directed mutagenesis strategies have been applied to plants for both *in vitro* as well

20    as *in vivo* site directed mutagenesis (Lanz *et al.*, *J. Biol. Chem. 266*:9971-9976 (1991), the entirety of which is herein incorporated by reference; Kovgan and Zhdanov, *Biotekhnologiya 5*:148-154, No. 207160n, Chemical Abstracts 110:225 (1989), the entirety of which is herein incorporated by reference; Ge *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 86*:4037-4041 (1989), the entirety of which is herein incorporated by reference; Zhu *et al.*, *J. Biol. Chem. 271*:18494-18498

25    (1996), the entirety of which is herein incorporated by reference; Chu *et al.*, *Biochemistry 33*:6150-6157 (1994), the entirety of which is herein incorporated by reference; Small *et al.*, *EMBO J. 11*:1291-1296 (1992), the entirety of which is herein incorporated by reference; Cho *et*

*al., Mol. Biotechnol. 8*:13-16 (1997), the entirety of which is herein incorporated by reference;

Kita *et al., J. Biol. Chem. 271*:26529-26535 (1996), the entirety of which is herein incorporated

by reference, Jin *et al., Mol. Microbiol. 7*:555-562 (1993), the entirety of which is herein

incorporated by reference; Hatfield and Vierstra, *J. Biol. Chem. 267*:14799-14803 (1992), the

5    entirety of which is herein incorporated by reference; Zhao *et al., Biochemistry 31*:5093-5099

(1992), the entirety of which is herein incorporated by reference).

Any of the nucleic acid molecules of the invention may either be modified by site directed

mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic

acid molecules for modification. It is understood that mutants with more than one altered

10   nucleotide can be constructed using techniques that practitioners are familiar with, such as

isolating restriction fragments and ligating such fragments into an expression vector (*see*, for

example, Sambrook *et al., Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press

(1989)).

Sequence-specific DNA-binding proteins play a role in the regulation of transcription.

15   The isolation of recombinant cDNAs encoding these proteins facilitates the biochemical analysis

of their structural and functional properties. Genes encoding such DNA-binding proteins have

been isolated using classical genetics (Vollbrecht *et al., Nature 350*: 241-243 (1991), the entirety

of which is herein incorporated by reference) and molecular biochemical approaches, including

the screening of recombinant cDNA libraries with antibodies (Landschulz *et al., Genes Dev.*

20   *2*:786-800 (1988), the entirety of which is herein incorporated by reference) or DNA probes

(Bodner *et al., Cell 55*:505-518 (1988), the entirety of which is herein incorporated by reference).

In addition, an *in situ* screening procedure has been used and has facilitated the isolation of

sequence-specific DNA-binding proteins from various plant species (Gilmartin *et al., Plant Cell*

*4*:839-849 (1992), the entirety of which is herein incorporated by reference; Schindler *et al.,*

25   *EMBO J. 11*:1261-1273 (1992), the entirety of which is herein incorporated by reference). An *in*

*situ* screening protocol does not require the purification of the protein of interest (Vinson *et al.,*

*Genes Dev.* 2:801-806 (1988), the entirety of which is herein incorporated by reference; Singh *et al., Cell* 52:415-423 (1988), the entirety of which is herein incorporated by reference).

Two steps may be employed to characterize DNA-protein interactions. The first is to identify sequence fragments that interact with DNA-binding proteins, to titrate binding activity,

5   to determine the specificity of binding and to determine whether a given DNA-binding activity can interact with related DNA sequences (Sambrook *et al., Molecular Cloning: A Laboratory Manual*, 2nd edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York (1989)). Electrophoretic mobility-shift assay is a widely used assay. The assay provides a rapid and sensitive method for detecting DNA-binding proteins based on the observation that the

10  mobility of a DNA fragment through a nondenaturing, low-ionic strength polyacrylamide gel is retarded upon association with a DNA-binding protein (Fried and Crother, *Nucleic Acids Res.* 9:6505-6525 (1981), the entirety of which is herein incorporated by reference). When one or more specific binding activities have been identified, the exact sequence of the DNA bound by the protein may be determined.

15  Several procedures for characterizing protein/DNA-binding sites are used, including methylation and ethylation interference assays (Maxam and Gilbert, *Methods Enzymol.* 65:499-560 (1980), the entirety of which is herein incorporated by reference; Wissman and Hillen, *Methods Enzymol.* 208:365-379 (1991), the entirety of which is herein incorporated by reference), footprinting techniques employing DNase I (Galas and Schmitz, *Nucleic Acids Res.*

20  5:3157-3170 (1978), the entirety of which is herein incorporated by reference), 1,10-phenanthroline-copper ion methods (Sigman *et al., Methods Enzymol.* 208:414-433 (1991), the entirety of which is herein incorporated by reference) and hydroxyl radicals methods (Dixon *et al., Methods Enzymol.* 208:414-433 (1991), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the invention may

25  be utilized to identify a protein or fragment thereof that specifically binds to a nucleic acid molecule of the invention. It is also understood that one or more of the protein molecules or

fragments thereof of the invention may be utilized to identify a nucleic acid molecule that specifically binds to it.

A two-hybrid system is based on the fact that proteins, such as transcription factors that interact (physically) with one another carry out many cellular functions. Two-hybrid systems have been used to probe the function of new proteins (Chien *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 88*:9578-9582 (1991) the entirety of which is herein incorporated by reference; Durfee *et al.*, *Genes Dev. 7*:555-569 (1993) the entirety of which is herein incorporated by reference; Choi *et al.*, *Cell 78*:499-512 (1994), the entirety of which is herein incorporated by reference; Kranz *et al.*, *Genes Dev. 8*:313-327 (1994), the entirety of which is herein incorporated by reference).

Interaction mating techniques have facilitated a number of two-hybrid studies of protein-protein interaction. Interaction mating has been used to examine interactions between small sets of tens of proteins (Finley and Brent, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:12098-12984 (1994), the entirety of which is herein incorporated by reference), larger sets of hundreds of proteins (Bendixen *et al.*, *Nucl. Acids Res. 22*:1778-1779 (1994), the entirety of which is herein incorporated by reference) and to comprehensively map proteins encoded by a small genome (Bartel *et al.*, *Nature Genetics 12*:72-77 (1996), the entirety of which is herein incorporated by reference). This technique utilizes proteins fused to the DNA-binding domain and proteins fused to the activation domain. They are expressed in two different haploid yeast strains of opposite mating type and the strains are mated to determine if the two proteins interact. Mating occurs when haploid yeast strains come into contact and result in the fusion of the two haploids into a diploid yeast strain. An interaction can be determined by the activation of a two-hybrid reporter gene in the diploid strain.

The CLONTECH laboratories, Inc. provides the MATCHMAKER two-hybrid System kit (Cat. No. K1605-1) in which the sequences encoding the two functional domains of the GAL4 transcriptional activator, DNA binding domain and activation domain, are cloned into two different shuttle/expression vectors (pGBT9 and pGAD424) ( Bartel *et al. In Cellular Interactions in Development: A Practical Approach*, D.A. Hartley, ed., Oxford University Press,

Oxford 153-179 (1993), the entirety of which is herein incorporated by reference). The gene

code for the target protein is cloned into the pGBT9 to generate a hybrid of GAL4-DNA binding

domain with a target protein and the gene(s) encode for potentially interacting protein(s) are

cloned into the pGAD424 to create hybrid protein(s) of GAL4-activation domain with potentially

5    interacting protein or with a collection of random proteins in a fusion library. The both plasmids

carrying hybrid proteins are cotransformed into one yeast strain. Both hybrid proteins are

targeted to the yeast nucleus by nuclear localization signal. If the target protein and the

potentially interacting protein interact with each other, the GAL4 DNA binding domain and the

GAL4 activation domain are brought to proximity and proper function of the transcriptional

10   activator unit will be reconstituted resulting in transcription of reporter gene (lacZ or HIS3). An

advantage of this technique is that it reduces the number of yeast transformations needed to test

individual interactions. It is understood that the protein-protein interactions of protein or

fragments thereof of the invention may be investigated using the two-hybrid system and that any

of the nucleic acid molecules of the invention that encode such proteins or fragments thereof may

15   be used to transform yeast in the two-hybrid system.

### (f)    Fungal Constructs and Fungal Transformants

The invention also relates to a fungal recombinant vector comprising exogenous genetic

material. The invention also relates to a fungal cell comprising a fungal recombinant vector.

The invention also relates to methods for obtaining a recombinant fungal host cell comprising

20   introducing into a fungal host cell exogenous genetic material.

Exogenous genetic material may be transferred into a fungal cell. In a preferred

embodiment the exogenous genetic material includes a nucleic acid molecule of the present

invention, preferably a nucleic acid molecule having a sequence selected from the group

consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragments of

25   either. Another preferred class of exogenous genetic material are nucleic acid molecules that

encode a protein having an amino acid selected from the group consisting of SEQ ID NO: 622

through SEQ ID NO: 626 or fragments thereof.

The fungal recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the fungal host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the fungal host.

The fungal vector may be an autonomously replicating vector, *i.e.,* a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.,* a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the fungal cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. This integration may be the result of homologous or non-homologous recombination.

Integration of a vector or nucleic acid into the genome by homologous recombination, regardless of the host being considered, relies on the nucleic acid sequence of the vector. Typically, the vector contains nucleic acid sequences for directing integration by homologous recombination into the genome of the host. These nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location or locations in one or more chromosomes. To increase the likelihood of integration at a precise location, there should be preferably two nucleic acid sequences that individually contain a sufficient number of nucleic acids, preferably 400bp to 1500bp, more preferably 800bp to 1000bp, which are highly homologous with the corresponding host cell target sequence. This enhances the probability of homologous recombination. These nucleic acid sequences may be any sequence that is homologous with a host cell target sequence and, furthermore, may or may not encode proteins.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of origin of replications for use in a yeast host cell are the 2 micron origin of replication and the combination

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of CEN3 and ARS 1. Any origin of replication may be used which is compatible with the fungal host cell of choice.

The fungal vectors of the invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs and the like. The selectable marker may be selected from the group including, but not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), hygB (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase) and *sC* (sulfate adenyltransferase) and *trpC* (anthranilate synthase). Preferred for use in an *Aspergillus* cell are the *amdS* and *pyrG* markers of *Aspergillus nidulans* or *Aspergillus oryzae* and the bar marker of *Streptomyces hygroscopicus*. Furthermore, selection may be accomplished by co-transformation, *e.g.*, as described in WO 91/17243, the entirety of which is herein incorporated by reference. A nucleic acid sequence of the invention may be operably linked to a suitable promoter sequence. The promoter sequence is a nucleic acid sequence which is recognized by the fungal host cell for expression of the nucleic acid sequence. The promoter sequence contains transcription and translation control sequences which mediate the expression of the protein or fragment thereof.

A promoter may be any nucleic acid sequence which shows transcriptional activity in the fungal host cell of choice and may be obtained from genes encoding polypeptides either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of a nucleic acid construct of the invention in a filamentous fungal host are promoters obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (glaA), *Rhizomucor miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Aspergillus nidulans* acetamidase and hybrids thereof. In a yeast host, a useful promoter is the *Saccharomyces cerevisiae* enolase (eno-1) promoter. Particularly preferred

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promoters are the TAKA amylase, NA2-tpi (a hybrid of the promoters from the genes encoding *Aspergillus niger* neutral alpha -amylase and *Aspergillus oryzae* triose phosphate isomerase), glaA, *Saccharomyces cerevisiae* GAL1 (galactokinase) and *Saccharomyces cerevisiae* GPD (glyceraldehyde-3-phosphate dehydrogenase) promoters.

5        A protein or fragment thereof encoding nucleic acid molecule of the invention may also be operably linked to a terminator sequence at its 3' terminus. The terminator sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any terminator which is functional in the fungal host cell of choice may be used in the invention, but particularly preferred terminators are obtained from the genes

10     encoding *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase, *Saccharomyces cerevisiae* cytochrome-c oxidase (CYC1) and *Saccharomyces cerevisiae* enolase.

       A protein or fragment thereof encoding nucleic acid molecule of the invention may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a

15     mRNA which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any leader sequence which is functional in the fungal host cell of choice may be used in the invention, but particularly preferred leaders are

20     obtained from the genes encoding *Aspergillus oryzae* TAKA amylase and *Aspergillus oryzae* triose phosphate isomerase.

       A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the invention. The polyadenylation sequence is a sequence which when transcribed is recognized by the fungal host to add polyadenosine residues to transcribed mRNA.

25     The polyadenylation sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any polyadenylation sequence which is functional in the fungal host of choice may be used in the invention, but particularly preferred

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polyadenylation sequences are obtained from the genes encoding *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase and *Saccharomyces cerevisiae* cytochrome-c oxidase (CYC1).

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof and to minimize the amount of possible degradation of the expressed protein or fragment thereof within the cell, it is preferred that expression of the protein or fragment thereof gives rise to a product secreted outside the cell. To this end, a protein or fragment thereof of the invention may be linked to a signal peptide linked to the amino terminus of the protein or fragment thereof. A signal peptide is an amino acid sequence which permits the secretion of the protein or fragment thereof from the fungal host into the culture medium. The signal peptide may be native to the protein or fragment thereof of the invention or may be obtained from foreign sources. The 5' end of the coding sequence of the nucleic acid sequence of the invention may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted protein or fragment thereof. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to that portion of the coding sequence which encodes the secreted protein or fragment thereof. The foreign signal peptide may be required where the coding sequence does not normally contain a signal peptide coding region. Alternatively, the foreign signal peptide may simply replace the natural signal peptide to obtain enhanced secretion of the desired protein or fragment thereof. The foreign signal peptide coding region may be obtained from a glucoamylase or an amylase gene from an *Aspergillus* species, a lipase or proteinase gene from *Rhizomucor miehei*, the gene for the alpha-factor from *Saccharomyces cerevisiae*, or the calf preprochymosin gene. An effective signal peptide for fungal host cells is the *Aspergillus oryzae* TAKA amylase signal, *Aspergillus niger* neutral amylase signal, the *Rhizomucor miehei* aspartic proteinase signal, the *Humicola lanuginosus* cellulase signal, or the *Rhizomucor miehei* lipase signal. However, any signal peptide capable of permitting secretion of the protein or fragment thereof in a fungal host of choice may be used in the invention.

A protein or fragment thereof encoding nucleic acid molecule of the invention may also

be linked to a propeptide coding region. A propeptide is an amino acid sequence found at the

amino terminus of aproprotein or proenzyme. Cleavage of the propeptide from the proprotein

yields a mature biochemically active protein. The resulting polypeptide is known as a

5      propolypeptide or proenzyme (or a zymogen in some cases). Propolypeptides are generally

inactive and can be converted to mature active polypeptides by catalytic or autocatalytic cleavage

of the propeptide from the propolypeptide or proenzyme. The propeptide coding region may be

native to the protein or fragment thereof or may be obtained from foreign sources. The foreign

propeptide coding region may be obtained from the *Saccharomyces cerevisiae* alpha-factor gene

10     or *Myceliophthora thermophila* laccase gene (WO 95/33836, the entirety of which is herein

incorporated by reference).

The procedures used to ligate the elements described above to construct the recombinant

expression vector of the invention are well known to one skilled in the art (see, for example,

Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual*, 2nd ed., Cold Spring Harbor, N.Y.,

15     (1989)).

The invention also relates to recombinant fungal host cells produced by the methods of

the invention which are advantageously used with the recombinant vector of the invention. The

cell is preferably transformed with a vector comprising a nucleic acid sequence of the invention

followed by integration of the vector into the host chromosome. The choice of fungal host cells

20     will to a large extent depend upon the gene encoding the protein or fragment thereof and its

source. The fungal host cell may, for example, be a yeast cell or a filamentous fungal cell.

"Yeast" as used herein includes *Ascosporogenous* yeast (*Endomycetales*),

*Basidiosporogenous* yeast and yeast belonging to the *Fungi Imperfecti* (*Blastomycetes*). The

*Ascosporogenous* yeasts are divided into the families *Spermophthoraceae* and

25     *Saccharomycetaceae*. The latter is comprised of four subfamilies, *Schizosaccharomycoideae* (for

example, genus *Schizosaccharomyces*), *Nadsonioideae*, *Lipomycoideae* and *Saccharomycoideae*

(for example, genera *Pichia, Kluyveromyces* and *Saccharomyces*). The *Basidiosporogenous*

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yeasts include the genera *Leucosporidim, Rhodosporidium, Sporidiobolus, Filobasidium* and

*Filobasidiella.* Yeast belonging to the *Fungi Imperfecti* are divided into two families,

*Sporobolomycetaceae* (for example, genera *Sorobolomyces* and *Bullera*) and *Cryptococcaceae*

(for example, genus *Candida*). Since the classification of yeast may change in the future, for the

5    purposes of this invention, yeast shall be defined as described in Biology and Activities of Yeast

(Skinner *et al., Soc. App. Bacteriol. Symposium Series* No. 9, (1980), the entirety of which is

herein incorporated by reference). The biology of yeast and manipulation of yeast genetics are

well known in the art (*see,* for example, *Biochemistry and Genetics of Yeast,* Bacil *et al.* (ed.),

2nd edition, 1987; *The Yeasts,* Rose and Harrison (eds.), 2nd ed., (1987); and *The Molecular*

10   *Biology of the Yeast Saccharomyces,* Strathern *et al.* (eds.), (1981), all of which are herein

incorporated by reference in their entirety).

"Fungi" as used herein includes the phyla *Ascomycota, Basidiomycota, Chytridiomycota*

and *Zygomycota* (as defined by Hawksworth *et al.,* In: Ainsworth and Bisby's *Dictionary of The*

*Fungi,* 8th edition, 1995, CAB International, University Press, Cambridge, UK; the entirety of

15   which is herein incorporated by reference) as well as the *Oomycota* (as cited in Hawksworth *et*

*al.,* In: Ainsworth and Bisby's *Dictionary of The Fungi,* 8th edition, 1995, CAB International,

University Press, Cambridge, UK) and all mitosporic fungi (Hawksworth *et al.,* In: Ainsworth

and Bisby's *Dictionary of The Fungi,* 8th edition, 1995, CAB International, University Press,

Cambridge, UK). Representative groups of *Ascomycota* include, for example, *Neurospora,*

20   *Eupenicillium* (= *Penicillium*), *Emericella* (= *Aspergillus*), *Eurotiun* (= *Aspergillus*) and the true

yeasts listed above. Examples of *Basidiomycota* include mushrooms, rusts and smuts.

Representative groups of *Chytridiomycota* include, for example, *Allomyces, Blastocladiella,*

*Coelomomyces* and aquatic fungi. Representative groups of *Oomycota* include, for example,

*Saprolegniomycetous* aquatic fungi (water molds) such as *Achlya.* Examples of mitosporic fungi

25   include *Aspergillus, Penicilliun, Candida* and *Alternaria.* Representative groups of *Zygomycota*

include, for example, *Rhizopus* and *Mucor.*

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"Filamentous fungi" include all filamentous forms of the subdivision *Eumycota* and

*Oomycota* (as defined by Hawksworth *et al.*, In: Ainsworth and Bisby's *Dictionary of The Fungi*,

8th edition, 1995, CAB International, University Press, Cambridge, UK). The filamentous fungi

are characterized by a vegetative mycelium composed of chitin, cellulose, glucan, chitosan,

5      mannan and other complex polysaccharides. Vegetative growth is by hyphal elongation and

carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as

*Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be

fermentative.

In one embodiment, the fungal host cell is a yeast cell. In a preferred embodiment, the

10     yeast host cell is a cell of the species of *Candida, Kluyveromyces, Saccharomyces,*

*Schizosaccharomyces, Pichia* and *Yarrowia.* In a preferred embodiment, the yeast host cell is a

*Saccharomyces cerevisiae* cell, a *Saccharomyces carlsbergensis, Saccharomyces diastaticus* cell,

a *Saccharomyces douglasii* cell, a *Saccharomyces kluyveri* cell, a *Saccharomyces norbensis* cell,

or a *Saccharomyces oviformis* cell. In another preferred embodiment, the yeast host cell is a

15     *Kluyveromyces lactis* cell. In another preferred embodiment, the yeast host cell is a *Yarrowia*

*lipolytica* cell.

In another embodiment, the fungal host cell is a filamentous fungal cell. In a preferred

embodiment, the filamentous fungal host cell is a cell of the species of, but not limited to,

*Acremonium, Aspergillus, Fusarium, Humicola, Myceliophthora, Mucor, Neurospora,*

20     *Penicillium, Thielavia, Tolypocladium* and *Trichoderma.*

The recombinant fungal host cells of the invention may further comprise one or more

sequences which encode one or more factors that are advantageous in the expression of the

protein or fragment thereof, for example, an activator (*e.g.*, a trans-acting factor), a chaperone

and a processing protease. The nucleic acids encoding one or more of these factors are

25     preferably not operably linked to the nucleic acid encoding the protein or fragment thereof. An

activator is a protein which activates transcription of a nucleic acid sequence encoding a

polypeptide (Kudla *et al., EMBO* 9:1355-1364(1990); Jarai and Buxton, *Current Genetics*

26:2238-244(1994); Verdier, *Yeast* 6:271-297(1990), all of which are herein incorporated by reference in their entirety). The nucleic acid sequence encoding an activator may be obtained from the genes encoding *Saccharomyces cerevisiae* heme activator protein 1 (hap1), *Saccharomyces cerevisiae* galactose metabolizing protein 4 (gal4) and *Aspergillus nidulans*

5　ammonia regulation protein (areA). For further examples, see Verdier, *Yeast* 6:271-297 (1990); MacKenzie *et al.*, *Journal of Gen. Microbiol.* 139:2295-2307 (1993), both of which are herein incorporated by reference in their entirety). A chaperone is a protein which assists another protein in folding properly (Hartl *et al.*, *TIBS* 19:20-25 (1994); Bergeron *et al.*, *TIBS* 19:124-128 (1994); Demolder *et al.*, *J. Biotechnology* 32:179-189 (1994); Craig, *Science* 260:1902-

10　1903(1993); Gething and Sambrook, *Nature* 355:33-45 (1992); Puig and Gilbert, *J Biol. Chem.* 269:7764-7771 (1994); Wang and Tsou, *FASEB Journal* 7:1515-11157 (1993); Robinson *et al.*, *Bio/Technology* 1:381-384 (1994), all of which are herein incorporated by reference in their entirety). The nucleic acid sequence encoding a chaperone may be obtained from the genes encoding *Aspergillus oryzae* protein disulphide isomerase, *Saccharomyces cerevisiae* calnexin,

15　*Saccharomyces cerevisiae* BiP/GRP78 and *Saccharomyces cerevisiae* Hsp70. For further examples, *see* Gething and Sambrook, *Nature* 355:33-45 (1992); Hartl *et al.*, *TIBS* 19:20-25 (1994). A processing protease is a protease that cleaves a propeptide to generate a mature biochemically active polypeptide (Enderlin and Ogrydziak, *Yeast* 10:67-79 (1994); Fuller *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.)* 86:1434-1438 (1989); Julius *et al.*, *Cell* 37:1075-1089 (1984);

20　Julius *et al.*, *Cell* 32:839-852 (1983), all of which are incorporated by reference in their entirety). The nucleic acid sequence encoding a processing protease may be obtained from the genes encoding *Aspergillus niger* Kex2, *Saccharomyces cerevisiae* dipeptidylaminopeptidase, *Saccharomyces cerevisiae* Kex2 and *Yarrowia lipolytica* dibasic processing endoprotease (xpr6). Any factor that is functional in the fungal host cell of choice may be used in the invention.

25　　　　Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts and regeneration of the cell wall in a manner known per se. Suitable procedures for transformation of *Aspergillus* host cells are described in EP 238 023 and

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Yelton *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 81*:1470-1474 (1984), both of which are herein incorporated by reference in their entirety. A suitable method of transforming *Fusarium* species is described by Malardier *et al.*, *Gene 78*:147-156 (1989), the entirety of which is herein incorporated by reference. Yeast may be transformed using the procedures described by Becker

5     and Guarente, In: Abelson and Simon, (eds.), *Guide to Yeast Genetics and Molecular Biology, Methods Enzymol.* Volume 194, pp. 182-187, Academic Press, Inc., New York; Ito *et al., J. Bacteriology 153*:163 (1983); Hinnen *et al., Proc. Natl. Acad. Sci. (U.S.A.) 75*:1920 (1978), all of which are herein incorporated by reference in their entirety.

The invention also relates to methods of producing the protein or fragment thereof

10    comprising culturing the recombinant fungal host cells under conditions conducive for expression of the protein or fragment thereof. The fungal cells of the invention are cultivated in a nutrient medium suitable for production of the protein or fragment thereof using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations)

15    in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the protein or fragment thereof to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art (*see, e.g.*, Bennett and LaSure (eds.), *More Gene Manipulations in Fungi*, Academic Press, CA, (1991), the entirety of which is herein

20    incorporated by reference). Suitable media are available from commercial suppliers or may be prepared according to published compositions (*e.g.*, in catalogues of the American Type Culture Collection, Manassas, VA). If the protein or fragment thereof is secreted into the nutrient medium, a protein or fragment thereof can be recovered directly from the medium. If the protein or fragment thereof is not secreted, it is recovered from cell lysates.

25    The expressed protein or fragment thereof may be detected using methods known in the art that are specific for the particular protein or fragment. These detection methods may include the use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme

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substrate. For example, if the protein or fragment thereof has enzymatic activity, an enzyme assay may be used. Alternatively, if polyclonal or monoclonal antibodies specific to the protein or fragment thereof are available, immunoassays may be employed using the antibodies to the protein or fragment thereof. The techniques of enzyme assay and immunoassay are well known

5      to those skilled in the art.

The resulting protein or fragment thereof may be recovered by methods known in the arts. For example, the protein or fragment thereof may be recovered from the nutrient medium by conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. The recovered protein or fragment thereof may then be

10     further purified by a variety of chromatographic procedures, *e.g.*, ion exchange chromatography, gel filtration chromatography, affinity chromatography, or the like.

### (g)    Mammalian Constructs and Transformed Mammalian Cells

The invention also relates to methods for obtaining a recombinant mammalian host cell, comprising introducing into a mammalian host cell exogenous genetic material. The invention

15     also relates to a mammalian cell comprising a mammalian recombinant vector. The invention also relates to methods for obtaining a recombinant mammalian host cell, comprising introducing into a mammalian cell exogenous genetic material. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention, preferably a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO: 1 through

20     SEQ ID NO: 621 or complements thereof or fragments of either. Another preferred class of exogenous genetic material are nucleic acid molecules that encode a protein having an amino acid selected from the group consisting of SEQ ID NO: 622 through SEQ ID NO: 626 or fragments thereof.

Mammalian cell lines available as hosts for expression are known in the art and include

25     many immortalized cell lines available from the American Type Culture Collection (ATCC, Manassas, VA), such as HeLa cells, Chinese hamster ovary (CHO) cells, baby hamster kidney (BHK) cells and a number of other cell lines.

Suitable promoters for mammalian cells are also known in the art and include viral promoters, such as those from Simian Virus 40 (SV40) (Fiers et al., Nature 273: 113 (1978)), Rous sarcoma virus (RSV), adenovirus (ADV), cytomegalovirus (CMV), and bovine papilloma virus (BPV), as well as mammalian cell-derived promoters. An exemplary, non-limiting, list

5    includes: a hematopoietic stem cell-specific promoter, such as the CD34 promoter (Burn et al., U.S. Patent No. 5,556,954); the glucose-6-phosphotase promoter (Yoshiuchi et al., J. Clin. Endocrin. Metab. 83:1016-1019 (1998)); interleukin-1 alpha promoter (Mori and Prager, Leuk. Lymphoma 26:421-433 (1997)); CMV promoter (Tong et al., Anticancer Res. 18:719-725 (1998), Norman et al., Vaccine 15:801-803 (1997)); RSV promoter (Elshami et al., Cancer Gene

10   Ther. 4:213-221 (1997); Baldwin et al., Gene Ther. 4:1142-1149 (1997)); SV40 promoter (Harms and Splitter, Hum. Gene Ther. 6:1291-1297 (1995)); CD11c integrin gene promoter (Corbi and Lopez-Rodriguez, Leuk. Lymphoma 25:415-425 (1997)), GM-CSF promoter (Shannon et al., Crit. Rev. Immunol. 17:301-323 (1997)); interleukin-5R alpha promoter (Sun et al., Curr. Top. Microbiol. Immunol 211:173-187 (1996)); interleukin-2 promoter (Serfing et al.,

15   Biochim. Biophys. Acta 1263:181-200 (1995); O'Neill et al., Transplant Proc. 23:2862-2866 (1991)); c-fos promoter (Janknecht, Immunobiology 193:137-142 (1995), Janknecht et al., Carcinogenesis 16:443-450 (1995), Takai et al., Princess Takamatsu Symp. 22:197-204 (1991)); h-ras promoter (Rachal et al., EXS 64:330-342 (1993)); and DMD gene promoter (Ray et al., Adv. Exp. Med. Biol. 280:107-111 (1990). All of the above documents are incorporated by

20   reference in their entirety and can be relied on to make or use aspects of this invention, especially in designing and constructing appropriate vector and host expression systems.

Vectors used in mammalian cell expression systems may also include additional functional sequences. For example, terminator sequences, poly-A addition sequences, and internal ribosome entry site (IRES) sequences. Enhancer sequences, which increase expression,

25   may also be included and sequences that promote amplification of the gene may also be desirable (for example, methotrexate resistance genes). One of skill in the art is familiar with numerous

examples of these additional functional sequences, as well as other functional sequences, that may optionally be included in an expression vector.

Vectors suitable for replication in mammalian cells may include viral replicons, or sequences which insure integration of the appropriate sequences encoding HCV epitopes into the host genome. For example, another vector used to express foreign DNA is vaccinia virus. In this case, for example, a nucleic acid molecule encoding a protein or fragment thereof is inserted into the vaccinia genome. Techniques for the insertion of foreign DNA into the vaccinia virus genome are known in the art and may utilize, for example, homologous recombination. Such heterologous DNA is generally inserted into a gene which is non-essential to the virus, for example, the thymidine kinase gene (tk), which also provides a selectable marker. Plasmid vectors that greatly facilitate the construction of recombinant viruses have been described (*see*, for example, Mackett *et al*, *J Virol.* *49*:857 (1984); Chakrabarti *et al.*, *Mol. Cell. Biol.* *5*:3403 (1985); Moss, In: *Gene Transfer Vectors For Mammalian Cells* (Miller and Calos, eds., Cold Spring Harbor Laboratory, N.Y., p. 10, (1987); all of which are herein incorporated by reference in their entirety). Expression of the HCV polypeptide then occurs in cells or animals which are infected with the live recombinant vaccinia virus.

The sequence to be integrated into the mammalian sequence may be introduced into the primary host by any convenient means, which includes calcium precipitated DNA, spheroplast fusion, transformation, electroporation, biolistics, lipofection, microinjection, or other convenient means. Where an amplifiable gene is being employed, the amplifiable gene may serve as the selection marker for selecting hosts into which the amplifiable gene has been introduced. Alternatively, one may include with the amplifiable gene another marker, such as a drug resistance marker, *e.g.*, neomycin resistance (G418 in mammalian cells), hygromycin in resistance etc., or an auxotrophy marker (HIS3, TRP1, LEU2, URA3, ADE2, LYS2, etc.) for use in yeast cells.

Depending upon the nature of the modification and associated targeting construct, various techniques may be employed for identifying targeted integration. Conveniently, the DNA may be

digested with one or more restriction enzymes and the fragments probed with an appropriate DNA fragment which will identify the properly sized restriction fragment associated with integration.

One may use different promoter sequences, enhancer sequences, or other sequence which will allow for enhanced levels of expression in the expression host. Thus, one may combine an enhancer from one source, a promoter region from another source, a 5'- noncoding region upstream from the initiation methionine from the same or different source as the other sequences and the like. One may provide for an intron in the non-coding region with appropriate splice sites or for an alternative 3'- untranslated sequence or polyadenylation site. Depending upon the particular purpose of the modification, any of these sequences may be introduced, as desired.

Where selection is intended, the sequence to be integrated will have with it a marker gene, which allows for selection. The marker gene may conveniently be downstream from the target gene and may include resistance to a cytotoxic agent, e.g., antibiotics, heavy metals, or the like, resistance or susceptibility to HAT, gancyclovir, etc., complementation to an auxotrophic host, particularly by using an auxotrophic yeast as the host for the subject manipulations, or the like. The marker gene may also be on a separate DNA molecule, particularly with primary mammalian cells. Alternatively, one may screen the various transformants, due to the high efficiency of recombination in yeast, by using hybridization analysis, PCR, sequencing, or the like.

For homologous recombination, constructs can be prepared where the amplifiable gene will be flanked, normally on both sides with DNA homologous with the DNA of the target region. Depending upon the nature of the integrating DNA and the purpose of the integration, the homologous DNA will generally be within 100kb, usually 50kb, preferably about 25kb, of the transcribed region of the target gene, more preferably within 2kb of the target gene. Where modeling of the gene is intended, homology will usually be present proximal to the site of the mutation. The homologous DNA may include the 5'-upstream region outside of the transcriptional regulatory region or comprising any enhancer sequences, transcriptional initiation

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sequences, adjacent sequences, or the like. The homologous region may include a portion of the coding region, where the coding region may be comprised only of an open reading frame or combination of exons and introns. The homologous region may comprise all or a portion of an intron, where all or a portion of one or more exons may also be present. Alternatively, the

5    homologous region may comprise the 3'-region, so as to comprise all or a portion of the transcriptional termination region, or the region 3' of this region. The homologous regions may extend over all or a portion of the target gene or be outside the target gene comprising all or a portion of the transcriptional regulatory regions and/or the structural gene.

The integrating constructs may be prepared in accordance with conventional ways, where

10   sequences may be synthesized, isolated from natural sources, manipulated, cloned, ligated, subjected to in vitro mutagenesis, primer repair, or the like. At various stages, the joined sequences may be cloned and analyzed by restriction analysis, sequencing, or the like. Usually during the preparation of a construct where various fragments are joined, the fragments, intermediate constructs and constructs will be carried on a cloning vector comprising a

15   replication system functional in a prokaryotic host, *e.g.*, *E. coli* and a marker for selection, *e.g.*, biocide resistance, complementation to an auxotrophic host, etc. Other functional sequences may also be present, such as polylinkers, for ease of introduction and excision of the construct or portions thereof, or the like. A large number of cloning vectors are available such as pBR322, the pUC series, etc. These constructs may then be used for integration into the primary

20   mammalian host.

In the case of the primary mammalian host, a replicating vector may be used. Usually, such vector will have a viral replication system, such as SV40, bovine papilloma virus, adenovirus, or the like. The linear DNA sequence vector may also have a selectable marker for identifying transfected cells. Selectable markers include the neo gene, allowing for selection

25   with G418, the herpes tk gene for selection with HAT medium, the gpt gene with mycophenolic acid, complementation of an auxotrophic host, etc.

The vector may or may not be capable of stable maintenance in the host. Where the vector is capable of stable maintenance, the cells will be screened for homologous integration of the vector into the genome of the host, where various techniques for curing the cells may be employed. Where the vector is not capable of stable maintenance, for example, where a

5     temperature sensitive replication system is employed, one may change the temperature from the permissive temperature to the non-permissive temperature, so that the cells may be cured of the vector. In this case, only those cells having integration of the construct comprising the amplifiable gene and, when present, the selectable marker, will be able to survive selection.

Where a selectable marker is present, one may select for the presence of the targeting

10     construct by means of the selectable marker. Where the selectable marker is not present, one may select for the presence of the construct by the amplifiable gene. For the neo gene or the herpes tk gene, one could employ a medium for growth of the transformants of about 0.1-1 mg/ml of G418 or may use HAT medium, respectively. Where DHFR is the amplifiable gene, the selective medium may include from about 0.01-0.5 μM of methotrexate or be deficient in

15     glycine-hypoxanthine-thymidine and have dialysed serum (GHT media).

The DNA can be introduced into the expression host by a variety of techniques that include calcium phosphate/DNA co-precipitates, microinjection of DNA into the nucleus, electroporation, yeast protoplast fusion with intact cells, transfection, polycations, *e.g.*, polybrene, polyornithine, etc., or the like. The DNA may be single or double stranded DNA,

20     linear or circular. The various techniques for transforming mammalian cells are well known (see Keown *et al.*, *Methods Enzymol.* (1989); Keown *et al.*, *Methods Enzymol. 185*:527-537 (1990); Mansour *et al.*, *Nature 336*:348-352, (1988); all of which are herein incorporated by reference in their entirety).

**(h)    Insect Constructs and Transformed Insect Cells**

25     The invention also relates to an insect recombinant vectors comprising exogenous genetic material. The invention also relates to an insect cell comprising an insect recombinant vector. The invention also relates to methods for obtaining a recombinant insect host cell, comprising

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introducing into an insect cell exogenous genetic material. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention, preferably a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragments of either. Another preferred class

5      of exogenous genetic material are nucleic acid molecules that encode a protein having an amino acid selected from the group consisting of SEQ ID NO: 622 through SEQ ID NO: 626 or fragments thereof.

The insect recombinant vector may be any vector which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleic acid sequence.

10     The choice of a vector will typically depend on the compatibility of the vector with the insect host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the insect host. In addition, the insect vector may be an expression vector. Nucleic acid molecules can be

15     suitably inserted into a replication vector for expression in the insect cell under a suitable promoter for insect cells. Many vectors are available for this purpose and selection of the appropriate vector will depend mainly on the size of the nucleic acid molecule to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or expression of DNA) and

20     the particular host cell with which it is compatible. The vector components for insect cell transformation generally include, but are not limited to, one or more of the following: a signal sequence, origin of replication, one or more marker genes and an inducible promoter.

The insect vector may be an autonomously replicating vector, *i.e.*, a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal

25     replication, *e.g.*, a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the insect cell, is integrated into the genome and

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replicated together with the chromosome(s) into which it has been integrated. For integration, the vector may rely on the nucleic acid sequence of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleic acid sequences for directing integration by homologous

5       recombination into the genome of the insect host. The additional nucleic acid sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, there should be preferably two nucleic acid sequences which individually contain a sufficient number of nucleic acids, preferably 400bp to 1500bp, more preferably 800bp to 1000bp, which are highly

10      homologous with the corresponding target sequence to enhance the probability of homologous recombination. These nucleic acid sequences may be any sequence that is homologous with a target sequence in the genome of the insect host cell and, furthermore, may be non-encoding or encoding sequences.

Baculovirus expression vectors (BEVs) have become important tools for the expression

15      of foreign genes, both for basic research and for the production of proteins with direct clinical applications in human and veterinary medicine (Doerfler, *Curr. Top. Microbiol. Immunol.* *131*:51-68 (1968); Luckow and Summers, *Bio/Technology* 6:47-55 (1988a); Miller, *Annual Review of Microbiol.* 42:177-199 (1988); Summers, *Curr. Comm. Molecular Biology*, Cold Spring Harbor Press, Cold Spring Harbor, N.Y. (1988); all of which are herein incorporated by

20      reference in their entirety). BEVs are recombinant insect viruses in which the coding sequence for a chosen foreign gene has been inserted behind a baculovirus promoter in place of the viral gene, *e.g.*, polyhedrin (Smith and Summers, U.S. Pat. No., 4,745,051, the entirety of which is incorporated herein by reference).

The use of baculovirus vectors relies upon the host cells being derived from *Lepidopteran*

25      insects such as *Spodoptera frugiperda* or *Trichoplusia ni*. The preferred *Spodoptera frugiperda* cell line is the cell line Sf9. The *Spodoptera frugiperda* Sf9 cell line was obtained from American Type Culture Collection (Manassas, VA.) and is assigned accession number ATCC

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CRL 1711 (Summers and Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,* Texas Ag. Exper. Station Bulletin No. 1555 (1988), the entirety of which is herein incorporated by reference). Other insect cell systems, such as the silkworm *B. mori* may also be used.

5     The proteins expressed by the BEVs are, therefore, synthesized, modified and transported in host cells derived from *Lepidopteran* insects. Most of the genes that have been inserted and produced in the baculovirus expression vector system have been derived from vertebrate species. Other baculovirus genes in addition to the polyhedrin promoter may be employed to advantage in a baculovirus expression system. These include immediate-early (alpha), delayed-early (β), late

10    (γ), or very late (delta), according to the phase of the viral infection during which they are expressed. The expression of these genes occurs sequentially, probably as the result of a "cascade" mechanism of transcriptional regulation. (Guarino and Summers, *J. Virol. 57*:563-571 (1986); Guarino and Summers, *J. Virol. 61*:2091-2099 (1987); Guarino and Summers, *Virol. 162*:444-451 (1988); all of which are herein incorporated by reference in their entirety).

15    Insect recombinant vectors are useful as intermediates for the infection or transformation of insect cell systems. For example, an insect recombinant vector containing a nucleic acid molecule encoding a baculovirus transcriptional promoter followed downstream by an insect signal DNA sequence is capable of directing the secretion of the desired biologically active protein from the insect cell. The vector may utilize a baculovirus transcriptional promoter region

20    derived from any of the over 500 baculoviruses generally infecting insects, such as for example the Orders *Lepidoptera, Diptera, Orthoptera, Coleoptera and Hymenoptera*, including for example but not limited to the viral DNAs of *Autographa californica MNPV, Bombyx mori NPV, Trichoplusia ni MNPV, Rachiplusia ou MNPV or Galleria mellonella MNPV,* wherein said baculovirus transcriptional promoter is a baculovirus immediate-early gene IE1 or IEN promoter;

25    an immediate-early gene in combination with a baculovirus delayed-early gene promoter region selected from the group consisting of 39K and a *HindIII-k* fragment delayed-early gene; or a baculovirus late gene promoter. The immediate-early or delayed-early promoters can be

enhanced with transcriptional enhancer elements. The insect signal DNA sequence may code for a signal peptide of a *Lepidopteran* adipokinetic hormone precursor or a signal peptide of the *Manduca sexta* adipokinetic hormone precursor (Summers, U.S. Patent No. 5,155,037; the entirety of which is herein incorporated by reference). Other insect signal DNA sequences include a signal peptide of the *Orthoptera Schistocerca gregaria* locust adipokinetic hormone precursor and the *Drosophila melanogaster* cuticle genes CP1, CP2, CP3 or CP4 or for an insect signal peptide having substantially a similar chemical composition and function (Summers, U.S. Patent No. 5,155,037).

Insect cells are distinctly different from animal cells. Insects have a unique life cycle and have distinct cellular properties such as the lack of intracellular plasminogen activators in which are present in vertebrate cells. Another difference is the high expression levels of protein products ranging from 1 to greater than 500 mg/liter and the ease at which cDNA can be cloned into cells (Frasier, *In Vitro Cell. Dev. Biol. 25*:225 (1989); Summers and Smith, In: *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,* Texas Ag. Exper. Station Bulletin No. 1555 (1988), both of which are incorporated by reference in their entirety).

Recombinant protein expression in insect cells is achieved by viral infection or stable transformation. For viral infection, the desired gene is cloned into baculovirus at the site of the wild-type polyhedron gene (Webb and Summers, *Technique 2*:173 (1990); Bishop and Posse, *Adv. Gene Technol. 1*:55 (1990); both of which are incorporated by reference in their entirety). The polyhedron gene is a component of a protein coat in occlusions which encapsulate virus particles. Deletion or insertion in the polyhedron gene results the failure to form occlusion bodies. Occlusion negative viruses are morphologically different from occlusion positive viruses and enable one skilled in the art to identify and purify recombinant viruses.

The vectors of invention preferably contain one or more selectable markers, which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides, for example biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs and the like. Selection may be accomplished by co-transformation, *e.g.*, as described in WO

91/17243, a nucleic acid sequence of the invention may be operably linked to a suitable promoter sequence. The promoter sequence is a nucleic acid sequence, which is recognized by the insect host cell for expression of the nucleic acid sequence. The promoter sequence contains transcription and translation control sequences, which mediate the expression of the protein or

5    fragment thereof. The promoter may be any nucleic acid sequence, which shows transcriptional activity in the insect host cell of choice and may be obtained from genes encoding polypeptides either homologous or heterologous to the host cell.

For example, a nucleic acid molecule encoding a protein or fragment thereof may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated region of a

10   mRNA, which is important for translation by the fungal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any leader sequence, which is functional in the insect host cell of choice may be used in the invention.

15   A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the invention. The polyadenylation sequence is a sequence which when transcribed is recognized by the insect host to add polyadenosine residues to transcribed mRNA. The polyadenylation sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any polyadenylation sequence,

20   which is functional in the fungal host of choice, may be used in the invention.

To avoid the necessity of disrupting the cell to obtain the protein or fragment thereof and to minimize the amount of possible degradation of the expressed polypeptide within the cell, it is preferred that expression of the polypeptide gene gives rise to a product secreted outside the cell. To this end, the protein or fragment thereof of the invention may be linked to a signal peptide

25   linked to the amino terminus of the protein or fragment thereof. A signal peptide is an amino acid sequence which permits the secretion of the protein or fragment thereof from the insect host into the culture medium. The signal peptide may be native to the protein or fragment thereof of

the invention or may be obtained from foreign sources. The 5' end of the coding sequence of the nucleic acid sequence of the invention may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted protein or fragment thereof.

At present, a mode of achieving secretion of a foreign gene product in insect cells is by way of the foreign gene's native signal peptide. Because the foreign genes are usually from non-insect organisms, their signal sequences may be poorly recognized by insect cells and, hence, levels of expression may be suboptimal. However, the efficiency of expression of foreign gene products seems to depend primarily on the characteristics of the foreign protein. On average, nuclear localized or non-structural proteins are most highly expressed, secreted proteins are intermediate and integral membrane proteins are the least expressed. One factor generally affecting the efficiency of the production of foreign gene products in a heterologous host system is the presence of native signal sequences (also termed presequences, targeting signals, or leader sequences) associated with the foreign gene. The signal sequence is generally coded by a DNA sequence immediately following (5' to 3') the translation start site of the desired foreign gene.

The expression dependence on the type of signal sequence associated with a gene product can be represented by the following example. If a foreign gene is inserted at a site downstream from the translational start site of the baculovirus polyhedrin gene so as to produce a fusion protein (containing the N-terminus of the polyhedrin structural gene), the fused gene is highly expressed. But less expression is achieved when a foreign gene is inserted in a baculovirus expression vector immediately following the transcriptional start site and totally replacing the polyhedrin structural gene.

Insertions into the region -50 to -1 significantly alter (reduce) steady state transcription which, in turn, reduces translation of the foreign gene product. Use of the pVL941 vector optimizes transcription of foreign genes to the level of the polyhedrin gene transcription. Even though the transcription of a foreign gene may be optimal, optimal translation may vary because

of several factors involving processing: signal peptide recognition, mRNA and ribosome binding, glycosylation, disulfide bond formation, sugar processing, oligomerization, for example.

The properties of the insect signal peptide are expected to be more optimal for the efficiency of the translation process in insect cells than those from vertebrate proteins. This phenomenon can generally be explained by the fact that proteins secreted from cells are synthesized as precursor molecules containing hydrophobic N-terminal signal peptides. The signal peptides direct transport of the select protein to its target membrane and are then cleaved by a peptidase on the membrane, such as the endoplasmic reticulum, when the protein passes through it.

Another exemplary insect signal sequence is the sequence encoding for Drosophila cuticle proteins such as CP1, CP2, CP3 or CP4 (Summers, U.S. Patent No. 5,278,050; the entirety of which is herein incorporated by reference). Most of a 9kb region of the Drosophila genome containing genes for the cuticle proteins has been sequenced. Four of the five cuticle genes contains a signal peptide coding sequence interrupted by a short intervening sequence (about 60 base pairs) at a conserved site. Conserved sequences occur in the 5' mRNA untranslated region, in the adjacent 35 base pairs of upstream flanking sequence and at -200 base pairs from the mRNA start position in each of the cuticle genes.

Standard methods of insect cell culture, cotransfection and preparation of plasmids are set forth in Summers and Smith (Summers and Smith, *A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures*, Texas Agricultural Experiment Station Bulletin No. 1555, Texas A&M University (1987)). Procedures for the cultivation of viruses and cells are described in Volkman and Summers, *J. Virol 19*:820-832 (1975) and Volkman *et al., J. Virol 19*:820-832 (1976); both of which are herein incorporated by reference in their entirety.

(i)     **Bacterial Constructs and Transformed Bacterial Cells**

The invention also relates to a bacterial recombinant vector comprising exogenous genetic material. The invention also relates to a bacteria cell comprising a bacterial recombinant vector. The invention also relates to methods for obtaining a recombinant bacteria host cell,

comprising introducing into a bacterial host cell exogenous genetic material. In a preferred embodiment the exogenous genetic material includes a nucleic acid molecule of the present invention, preferably a nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof or fragments of either. Another preferred class of exogenous genetic material are nucleic acid molecules that encode a protein having an amino acid selected from the group consisting of SEQ ID NO: 622 through SEQ ID NO: 626 or fragments thereof.

The bacterial recombinant vector may be any vector that can be conveniently subjected to recombinant DNA procedures. The choice of a vector will typically depend on the compatibility of the vector with the bacterial host cell into which the vector is to be introduced. The vector may be a linear or a closed circular plasmid. The vector system may be a single vector or plasmid or two or more vectors or plasmids, which together contain the total DNA to be introduced into the genome of the bacterial host. In addition, the bacterial vector may be an expression vector. Nucleic acid molecules encoding protein homologues or fragments thereof can, for example, be suitably inserted into a replicable vector for expression in the bacterium under the control of a suitable promoter for bacteria. Many vectors are available for this purpose and selection of the appropriate vector will depend mainly on the size of the nucleic acid to be inserted into the vector and the particular host cell to be transformed with the vector. Each vector contains various components depending on its function (amplification of DNA or expression of DNA) and the particular host cell with which it is compatible. The vector components for bacterial transformation generally include, but are not limited to, one or more of the following: a signal sequence, an origin of replication, one or more marker genes and an inducible promoter.

In general, plasmid vectors containing replicon and control sequences that are derived from species compatible with the host cell are used in connection with bacterial hosts. The vector ordinarily carries a replication site, as well as marking sequences that are capable of providing phenotypic selection in transformed cells. For example, *E. coli* is typically

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transformed using pBR322, a plasmid derived from an *E. coli* species (see, *e.g.*, Bolivar *et al.*, *Gene* 2:95 (1977); the entirety of which is herein incorporated by reference). The plasmid pBR322 contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid or phage,

5    also generally contains, or is modified to contain, promoters that can be used by the microbial organism for expression of the selectable marker genes.

Nucleic acid molecules encoding protein or fragments thereof may be expressed not only directly, but also as a fusion with another polypeptide, preferably a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature polypeptide. In

10    general, the signal sequence may be a component of the vector, or it may be a part of the polypeptide DNA that is inserted into the vector. The heterologous signal sequence selected should be one that is recognized and processed (*i.e.*, cleaved by a signal peptidase) by the host cell. For bacterial host cells that do not recognize and process the native polypeptide signal sequence, the signal sequence is substituted by a bacterial signal sequence selected, for example,

15    from the group consisting of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Generally, in cloning vectors this sequence is one that enables the vector to replicate independently of the host chromosomal DNA and

20    includes origins of replication or autonomously replicating sequences. Such sequences are well known for a variety of bacteria. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria.

Expression and cloning vectors also generally contain a selection gene, also termed a selectable marker. This gene encodes a protein necessary for the survival or growth of

25    transformed host cells grown in a selective culture medium. Host cells not transformed with the vector containing the selection gene will not survive in the culture medium. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, *e.g.*, ampicillin,

neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, *e.g.*, the gene encoding D-alanine racemase for *Bacilli*. One example of a selection scheme utilizes a drug to arrest growth of a host cell. Those cells that are successfully transformed with a heterologous protein homologue or fragment

5    thereof produce a protein conferring drug resistance and thus survive the selection regimen.

The expression vector for producing a protein or fragment thereof can also contains an inducible promoter that is recognized by the host bacterial organism and is operably linked to the nucleic acid encoding, for example, the nucleic acid molecule encoding the protein homologue or fragment thereof of interest. Inducible promoters suitable for use with bacterial hosts include the

10    β-lactamase and lactose promoter systems (Chang *et al.*, *Nature 275*:615 (1978); Goeddel *et al.*, *Nature 281*:544 (1979); both of which are herein incorporated by reference in their entirety), the arabinose promoter system (Guzman *et al.*, *J. Bacteriol. 174*:7716-7728 (1992); the entirety of which is herein incorporated by reference), alkaline phosphatase, a tryptophan (trp) promoter system (Goeddel, *Nucleic Acids Res. 8*:4057 (1980); EP 36,776; both of which are herein

15    incorporated by reference in their entirety) and hybrid promoters such as the tac promoter (deBoer *et al.*, *Proc. Natl. Acad. Sci. (USA) 80*:21-25 (1983); the entirety of which is herein incorporated by reference). However, other known bacterial inducible promoters are suitable (Siebenlist *et al.*, *Cell 20*:269 (1980); the entirety of which is herein incorporated by reference).

Promoters for use in bacterial systems also generally contain a Shine-Dalgarno (S.D.)

20    sequence operably linked to the DNA encoding the polypeptide of interest. The promoter can be removed from the bacterial source DNA by restriction enzyme digestion and inserted into the vector containing the desired DNA.

Construction of suitable vectors containing one or more of the above-listed components employs standard ligation techniques. Isolated plasmids or DNA fragments are cleaved, tailored

25    and re-ligated in the form desired to generate the plasmids required. Examples of available bacterial expression vectors include, but are not limited to: the multifunctional *E. coli* cloning and expression vectors such as Bluescript™ (Stratagene, La Jolla, CA), in which, for example,

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encoding an A. *nidulans* protein homologue or fragment thereof homologue, may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of β-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke and Schuster, *J. Biol. Chem. 264*:5503-5509 (1989), the entirety of which is herein incorporated by reference);

5    and the like. pGEX vectors (Promega, Madison Wisconsin U.S.A.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems are designed to optionally include a heparin, thrombin, or factor XA protease

10   cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will. Proteins or polypeptides of the invention can be expressed as variants that facilitate purification. For example, a fusion protein to such proteins as maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX) are known in the art [New England BioLab, Beverly, Mass., Pharmacia, Piscataway, NJ, and InVitrogen, San Diego, CA]. The

15   polypeptide or protein can also be a tagged variant to facilitate purification, such as with histidine or methionine rich regions (His-Tag; available from LifeTechnologies Inc, Gaithersburg, MD) that bind to metal ion affinity chromatography columns, or with an epitope that binds to a specific antibody (Flag, available from Kodak, New Haven, Conn.). An exemplary, non-limiting list of commercially available vectors suitable for fusion protein expression includes: pBR322

20   (Promega); pGEX (Amersham); pT7 (USB); pET (Novagen); pIBI (IBI); pProEX-1 (Gibco/BRL); pBluescript II (Stratagene); pTZ18R and pTZ19R (USB); pSE420 (Invitrogen); pVL1392 (Invitrogen); pBlueBac (Invitrogen); pBAcPAK (Clontech); pHIL (Invitrogen); pYES2 (Invitrogen); pCDNA (Invitrogen); and pREP (Invitrogen). A number of other purification methods or means are also known and can be used. Reverse-phase high performance liquid

25   chromatography (RP-HPLC), optionally employing hydrophobic RP-HPLC media, *e.g.*, silica gel, further purify the protein. Combinations of methods and means can also be employed to provide a substantially purified recombinant polypeptide or protein. Isolated plasmids or DNA

fragments are cleaved, tailored, and re-ligated in the form desired to generate the plasmids required. Examples of available bacterial expression vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as Bluescript Registered TM (Stratagene, La Jolla, CA), in which, for example, encoding an gene homologue or fragment thereof homologue, may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of beta -galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke and Schuster *J. Biol. Chem. 264*: 5503-5509 (1989). The entirety of which is herein incorporated by reference); and the like. pGEX vectors (Promega, Madison Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems are designed to include heparin, thrombin or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

Suitable host bacteria for a bacterial vector include archaebacteria and eubacteria, especially eubacteria and most preferably *Enterobacteriaceae*. Examples of useful bacteria include *Escherichia, Enterobacter, Azotobacter, Erwinia, Bacillus, Pseudomonas, Klebsiella, Proteus, Salmonella, Serratia, Shigella, Rhizobia, Vitreoscilla and Paracoccus*. Suitable *E. coli* hosts include *E. coli* W3110 (American Type Culture Collection (ATCC) 27,325, Manassas, Virginia U.S.A.), *E. coli* 294 (ATCC 31,446), *E. coli* B and *E. coli* X1776 (ATCC 31,537). These examples are illustrative rather than limiting. Mutant cells of any of the above-mentioned bacteria may also be employed. It is, of course, necessary to select the appropriate bacteria taking into consideration replicability of the replicon in the cells of a bacterium. For example, *E. coli, Serratia,* or *Salmonella* species can be suitably used as the host when well known plasmids such as pBR322, pBR325, pACYC177, or pKN410 are used to supply the replicon. *E. coli* strain W3110 is a preferred host or parent host because it is a common host strain for recombinant

DNA product fermentations. Preferably, the host cell should secrete minimal amounts of proteolytic enzymes.

Host cells are transfected and preferably transformed with the above-described vectors and cultured in conventional nutrient media modified as appropriate for inducing promoters, 5 selecting transformants, or amplifying the genes encoding the desired sequences.

Numerous methods of transfection are known to the ordinarily skilled artisan, for example, calcium phosphate and electroporation. Depending on the host cell used, transformation is done using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in section 1.82 of Sambrook *et al.*, 10 *Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Laboratory Press, (1989), is generally used for bacterial cells that contain substantial cell-wall barriers. Another method for transformation employs polyethylene glycol/DMSO, as described in Chung and Miller (Chung and Miller, *Nucleic Acids Res. 16*:3580 (1988); the entirety of which is herein incorporated by reference). Yet another method is the use of the technique termed 15 electroporation.

Bacterial cells used to produce the polypeptide of interest for purposes of this invention are cultured in suitable media in which the promoters for the nucleic acid encoding the heterologous polypeptide can be artificially induced as described generally, *e.g.*, in Sambrook *et al., Molecular Cloning: A Laboratory Manual*, New York: Cold Spring Harbor Laboratory Press, 20 (1989). Examples of suitable media are given in U.S. Pat. Nos. 5,304,472 and 5,342,763; both of which are incorporated by reference in their entirety.

In addition to the above discussed procedures, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (*e.g.*, DNA molecules, plasmids, etc.), generation 25 of recombinant organisms and the screening and isolating of clones, (see for example, Sambrook *et al., Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989); Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995), the entirety of which

is herein incorporated by reference; Birren *et al., Genome Analysis: Analyzing DNA,* 1, Cold

Spring Harbor, New York, the entirety of which is herein incorporated by reference).

### (j)     Algal Constructs and Algal Transformants

The present invention also relates to an algal recombinant vector comprising exogenous

5      genetic material.  The present invention also relates to an algal cell comprising an algal

recombinant vector.  The present invention also relates to methods for obtaining a recombinant

algal host cell comprising introducing into an algal host cell exogenous genetic material.

Exogenous genetic material is any genetic material, whether naturally occurring or

otherwise, from any source that is capable of being inserted into any organism.  Exogenous

10     genetic material may be transferred into an algal cell.  In a preferred embodiment the exogenous

genetic material includes a nucleic acid molecule having a sequence selected from the group

consisting of SEQ ID NO: 1 through SEQ ID NO: 621 or complements thereof.  Another

preferred class of exogenous genetic material are nucleic acid molecules that encode a protein

having an amino acid selected from the group consisting of SEQ ID NO: 622 through SEQ ID

15     NO: 626 or fragments thereof.

The algal recombinant vector may be any vector which can be conveniently subjected to

recombinant DNA procedures.  The choice of a vector will typically depend on the compatibility

of the vector with the algal host cell into which the vector is to be introduced.  The vector may be

a linear or a closed circular plasmid.  The vector system may be a single vector or plasmid or two

20     or more vectors or plasmids which together contain the total DNA to be introduced into the

genome of the algal host.

The algal vector may be an autonomously replicating vector, *i.e.,* a vector which exists as

an extrachromosomal entity, the replication of which is independent of chromosomal replication,

*e.g.,* a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

25     The vector may contain any means for assuring self-replication.  Alternatively, the vector may be

one which, when introduced into the algal cell, is integrated into the genome and replicated

together with the chromosome(s) into which it has been integrated.  For integration, the vector

may rely on the nucleic acid sequence of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleic acid sequences for directing integration by homologous recombination into the genome of the algal host. The additional nucleic acid sequences enable the vector to be

5    integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, there should be preferably two nucleic acid sequences which individually contain a sufficient number of nucleic acids, preferably 400 bp to 1500 bp, more preferably 800 bp to 1000 bp, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. These

10   nucleic acid sequences may be any sequence that is homologous with a target sequence in the genome of the algal host cell, and, furthermore, may be non-encoding or encoding sequences.

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene, the product of which confers upon an algal cell resistance to a compound to which the algal would otherwise be

15   sensitive. The compound can be selected from the group consisting of antibiotics, fungicides, herbicides, and heavy metals. The selectable marker may be selected from any known or subsequently identified selectable markers, including markers derived from algal, fungal, and bacterial sources. Preferred selectable markers can be selected from the group including, but not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin

20   acetyltransferase), *ble* (bleomycin binding protein), *cat* (chloramphenicol acetyltransferase), hygB (hygromycin B phosphotransferase), *nat* (nourseothricin acetyltransferase), *niaD* (nitrate reductase), *neo* (neomycin phosphotransferase), *pac* (puromycin acetyltransferase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sat* (streptothricin acetyltransferase), *sC* (sulfate adenyltransferase), *trpC* (anthranilate synthase), and glyphosate resistant EPSPS genes.

25   Furthermore, selection may be accomplished by co-transformation, *e.g.*, as described in WO 91/17243, herein incorporated by reference in its entirety.

A nucleic acid sequence of the present invention may be operably linked to a suitable promoter sequence. The promoter sequence is a nucleic acid sequence which is recognized by the algal host cell for expression of the nucleic acid sequence. The promoter sequence contains transcription and translation control sequences which mediate the expression of the protein or

5    fragment thereof.

A promoter may be any nucleic acid sequence which shows transcriptional activity in the algal host cell of choice and may be obtained from genes encoding polypeptides either homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of a nucleic acid construct of the invention in an algal host are light harvesting

10   protein promoters obtained from photosynthetic organisms, *Chlorella* virus methyltransferase promoters, CaMV 35 S promoter, PL promoter from bacteriophage λ, nopaline synthase promoter from the Ti plasmid of *Agrobacterium tumefaciens*, and bacterial trp promoter.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a terminator sequence at its 3' terminus. The terminator sequence

15   may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any terminator which is functional in the algal host cell of choice may be used in the present invention.

A protein or fragment thereof encoding nucleic acid molecule of the present invention may also be operably linked to a suitable leader sequence. A leader sequence is a nontranslated

20   region of a mRNA which is important for translation by the algal host. The leader sequence is operably linked to the 5' terminus of the nucleic acid sequence encoding the protein or fragment thereof. The leader sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any leader sequence which is functional in the algal host cell of choice may be used in the present invention.

25   A polyadenylation sequence may also be operably linked to the 3' terminus of the nucleic acid sequence of the present invention. The polyadenylation sequence is a sequence which when transcribed is recognized by the algal host to add polyadenosine residues to transcribed mRNA.

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The polyadenylation sequence may be native to the nucleic acid sequence encoding the protein or fragment thereof or may be obtained from foreign sources. Any polyadenylation sequence which is functional in the algal host of choice may be used in the present invention.

The procedures used to ligate the elements described above to construct the recombinant expression vector of the present invention are well known to one skilled in the art (see, for example, Sambrook, 2nd ed., *et al.*, *Molecular Cloning, A Laboratory Manual Cold Spring Harbor, N.Y.*, (1989), herein incorporated by reference in its entirety).

The present invention also relates to recombinant algal host cells produced by the methods of the present invention which are advantageously used with the recombinant vector of the present invention. The cell is preferably transformed with a vector comprising a nucleic acid sequence of the invention followed by integration of the vector into the host chromosome. The choice of algal host cells will to a large extent depend upon the gene encoding the protein or fragment thereof and its source.

Algal cells may be transformed by a variety of known techniques, including but not limit to, microprojectile bombardment, protoplast fusion, electroporation, microinjection, and vigorous agitation in the presence of glass beads. Suitable procedures for transformation of green algal host cells are described in EP 108 580, herein incorporated by reference in its entirety. A suitable method of transforming *Chlorella* species is described by Jarvis and Brown, Curr. *Genet. 19:* 317-321 (1991), herein incorporated by reference in its entirety. A suitable method of transforming cells of diatom *Phaeodactylum tricornutum* species is described in WO 97/39106, herein incorporated by reference in its entirety. Chlorophyll C-containing algae may be transformed using the procedures described in US 5,661,017, herein incorporated by reference in its entirety.

The expressed protein or fragment thereof may be detected using methods known in the art that are specific for the particular protein or fragment. These detection methods may include the use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, if the protein or fragment thereof has enzymatic activity, an enzyme

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assay may be used. Alternatively, if polyclonal or monoclonal antibodies specific to the protein or fragment thereof are available, immunoassays may be employed using the antibodies to the protein or fragment thereof. The techniques of enzyme assay and immunoassay are well known to those skilled in the art.

5        The resulting protein or fragment thereof may be recovered by methods known in the arts. For example, the protein or fragment thereof may be recovered from the nutrient medium by conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. The recovered protein or fragment thereof may then be further purified by a variety of chromatographic procedures, e.g., ion exchange chromatography,

10      gel filtration chromatography, affinity chromatography, or the like.

**Computer Readable Media**

        The nucleotide or amino acid sequence provided in SEQ ID NO: 1 through SEQ ID NO: 626, or fragment thereof, or complement thereof, or a nucleotide or an amino acid sequence at least 70% identical, preferably 90% identical even more preferably 99% or about 100% identical

15      to the sequence provided in SEQ ID NO: 1 through SEQ ID NO: 626, or where appropriate complement thereof or fragments of either, can be "provided" in a variety of mediums to facilitate use. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences.

        A further preferred subset of nucleic acid sequences is where the subset of sequences is

20      two proteins or fragments thereof, more preferably three proteins or fragments thereof and even more preferable four proteins or fragments thereof.

        In one application of this embodiment, a nucleotide sequence of the invention can be recorded on computer readable media so that a computer–readable medium comprises one or more of the nucleotide sequences of the invention. As used herein, "computer readable media"

25      refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium

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and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

Any number of the sequences, or sequence fragments, of the nucleic acid molecules or proteins of the invention, or fragments of either, can be included, in any number of combinations, on a computer-readable medium. Specifically, any one or more of SEQ ID NO:1-626, or where appropriate, complements thereof, can be included.

A skilled artisan can readily appreciate how any computer readable medium can be used to create a machine or method comprising a computer readable medium having recorded thereon a nucleotide sequence of the invention. As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any method for recording information on computer readable medium to generate media comprising the nucleotide sequence information of the invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect or Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.,* text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the invention.

By providing one or more of nucleotide sequences of the invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available that allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990), the entirety of which

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is herein incorporated by reference) and BLAZE (Brutlag *et al., Comp. Chem. 17:*203-207 (1993), the entirety of which is herein incorporated by reference) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding

5    fragments within the sequences of the invention and are useful in producing commercially important proteins such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification and DNA replication, restriction, modification, recombination and repair.

The invention further provides systems, particularly computer-based systems, which

10    contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the invention. As used herein, "a computer-based system" refers to the hardware means, software means and data storage means used to analyze the nucleotide sequence information of the invention. The minimum hardware means of the computer-based systems of the invention comprises a central processing unit

15    (CPU), input means, output means and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the invention.

As indicated above, the computer-based systems of the invention comprise a data storage means having stored therein a nucleotide sequence of the invention and the necessary hardware

20    means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target

25    sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the invention that match a particular target sequence or target motif. A variety of known algorithms are

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disclosed publicly and a variety of commercially available software for conducting search means are available can be used in the computer-based systems of the invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequences the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the invention sequence identified using a search means as described above and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the invention. A preferred format for an output means ranks fragments of the sequence of the invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments sequence of the invention. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990)) can be used to identify open frames within the nucleic acid molecules of the invention. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the invention.

Having now described the invention, the following examples are provided by way of illustration and are not intended to limit the scope of the invention, unless specified.

## Example 1

**Identification of Yeast HES1**

The yeast strain LPY9 (MATa, leu2, Ura3, his3) is grown overnight and inoculated into SD+ hul (histidine, uracil, leucine) media. Aliquots of the culture are treated with ketoconazole (an inhibitor of C-14α demethylase ($P450_{14DM}$) enzyme) at 10ug/ml, 50ug/ml, and 100ug/ml, corresponding to 10ppm, 50ppm, and 100ppm, respectively. A sample of each is collected at 2, 4, and 6 hours after treatment. Control samples treated with DMSO (dimethyl sulfoxide-solvent for ketoconazole) but not with ketoconazole are also collected. Total RNA from each sample is collected by conventional methods, such as a Zirconium/Silica bead binding and extraction method. The sequence content of each sample is analyzed and compared by hybridizing each of them to a number of yeast ORF sequences immobilized on a Nylon membrane in an array format.

A similar comparison of a wild type yeast strain and a double mutant strain is made. The double mutant CJ517 (MATa, erg11::URA3, erg3::LEU2, leu2, ura3, his4) [erg11, erg3 double mutant] is compared to LPY9 after growth in both YPD and SD+hul media. Samples are collected at approximately 0, 2, 4, and 6 hours after inoculation.

Table 2, below, lists the RNAs in each sample whose abundance is effected by ketoconazole treatment or whose abundance differs between wild type and the double mutant strain. The table also lists the corresponding gene or sequence identifier for those RNAs. The RNAs are ranked by the ratio of either ketocanozole vs. control or mutant vs. control, using the ratio of 50ppm ketocanozole/control as a basis for comparison.

**Table 2\***

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 30 | YOR237W | (HES1) | 134.648161 | 1417.6262 | 1358.1235 | Protein implicated in ergosterol biosynthesis, member of the KES1/HES1/OSH1/YKR003W family of oxysterol-binding (OSBP) proteins |
| 31 | YKL198C | (PTK1) | 68.5845326 | 111.1984 | 233.11762 | Serine/threonine protein kinase, activator of low-affinity, low-capacity polyamine transport |
| 32 | YLR465C | - | 97.9601498 | 104.52215 | 133.57826 | Protein of unknown function, questionable ORF |
| 33 | YMR129W | (POM152) | 5.10206225 | 82.813831 | 15.392788 | Nuclear pore membrane glycoprotein, type II integral membrane protein with N-terminal region on pore side and C-terminal region in the cisternae |
| 34 | YBR284W | - | 4.92774291 | 60.027955 | 8.5359554 | Protein with similarity to AMP deaminase |
| 35 | YKL158W | - | 11.6717854 | 59.827307 | 75.220412 | Protein of unknown function |
| 36 | YOR083W | - | 31.7378598 | 51.606081 | 42.301568 | Protein of unknown function |
| 37 | YOL095C | - | 3.60507866 | 49.740211 | 21.834188 | Protein with similarity to S. aureus DNA helicase PCRA |
| 38 | YOR188W | (MSB1) | 2.19997209 | 42.446767 | 61.303817 | Protein that may play a role in polarity establishment and bud formation |
| 39 | YBL109W | - | 0.08616121 | 38.653463 | 75.964757 | - |
| 40 | YLR091W | - | 17.5946744 | 38.325073 | 44.556481 | Protein of unknown function |
| 41 | YNL106C | (INP52) | 2.52986454 | 35.205536 | 17.376557 | - |
| 42 | YDR213W | - | 18.2079478 | 32.136065 | 58.358612 | Protein with similarity to transcription factors, has ZN[2]-CYS[6] fungal-type binuclear cluster domain in the N-terminal region |
| 43 | YBL004W | - | 8.49387973 | 28.614573 | 28.645633 | Protein with similarity to members of the major facilitator superfamily (MFS) |
| 44 | YIR019C | (MUC1) | 48.7538739 | 27.594853 | 137.77885 | Glucoamylase I (alpha-1,4-glucan glucosidase), extracellular enzyme |
| 45 | YJL182C | - | 2.53469593 | 26.891434 | 29.499298 | Protein of unknown function |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 46 | YMR254C | - | 0.19897977 | 26.633459 | 10.625738 | Protein of unknown function, questionable ORF |
| 47 | YDL134C | (PPH21) | 3.51284473 | 22.849241 | 0 | - |
| 48 | YCR098C | (GIT1) | 2.27672091 | 21.746838 | 24.724171 | Protein involved in inositol metabolism |
| 49 | YPL150W | - | 4.72964069 | 21.633895 | 34.40982 | Serine/threonine protein kinase of unknown function |
| 50 | YKL110C | (KTI12) | 19.7752946 | 21.085633 | 16.303432 | Protein involved in resistance to kluyveromyces lactis killer toxin |
| 51 | YER011W | (TIR1) | 31.4723195 | 20.454605 | 17.935906 | Stress-induced cell wall structural protein of the PAU1 family |
| 52 | YDL024C | - | 3.96163383 | 20.381493 | 30.488098 | Protein with similarity to acid phosphatases |
| 53 | YGR013W | - | 0.10491681 | 20.364081 | 0 | - |
| 54 | YOR325W | - | 47.3518002 | 20.211317 | 29.305064 | Protein of unknown function |
| 55 | YJR150C | - | 159.265973 | 19.793221 | 13.560079 | - |
| 56 | YDL126C | (CDC48) | 42.7590386 | 19.0472 | 15.014024 | Protein of the AAA family of ATPases, required for cell division and homotypic membrane fusion |
| 57 | YLR464W | - | 12.4297115 | 18.580843 | 36.516503 | Protein with similarity to other subtelomerically-coded proteins |
| 58 | YLR124W | - | 0.13902212 | 18.351487 | 11.026125 | Protein of unknown function |
| 59 | YLR463C | - | 8.49721471 | 18.007814 | 29.811632 | Protein with similarity to other subtelomerically-coded proteins |
| 60 | YMR297W | (PRC1) | 6.20117404 | 17.995865 | 24.291751 | Carboxypeptidase Y (CPY) (YSCY), serine-type protease |
| 61 | YFL029C | (CAK1) | 17.1104765 | 16.96782 | 44.352291 | CDK-activating kinase (serine/threonine protein kinase) responsible for in vivo activation of CDC28P, also involved in spore wall formation |
| 62 | YER054C | (GIP2) | 2.14214491 | 16.442373 | 15.284537 | GLC7P-interacting protein, possible regulatory subunit for the PP1 family protein phosphatase GLC7P |
| 63 | YER060W-A | (FCY22) | 2.61677424 | 15.768882 | 20.550953 | Purine-cytosine permease with similarity to FCY2P, member of the purine/cytosine family of the major facilitator superfamily (MFS) |
| 64 | YEL076C | - | 13.7918147 | 14.372278 | 26.325282 | Protein with similarity to other subtelomerically-encoded proteins |
| 65 | YGL176C | - | 9.0823019 | 14.17085 | 16.23816 | Protein with similarity to discopyge OMMATA CA++ channel alpha1 subunit protein B47447 |
| 66 | YNR005C | - | 12.9230524 | 14.032659 | 13.011356 | Protein of unknown function, questionable ORF |
| 67 | YML032C-A | - | 6.92372404 | 13.847081 | 5.501802 | - |
| 68 | YGR190C | - | 22.9885796 | 13.701633 | 42.22779 | Protein of unknown function |
| 69 | YHR213W | - | 17.3140804 | 13.267403 | 21.010074 | Protein with similarity to the N-terminus of FLO1P and identical to YAR062P, probable pseudogene |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 70 | YPL272C | - | 24.778114 | 12.93877 | 11.647985 | Protein of unknown function |
| 71 | YBL100C | - | 4.8456884 | 12.432421 | 16.193059 | Protein of unknown function |
| 72 | YLR024C | - | 11.2130442 | 11.927798 | 17.73046 | Protein with similarity to ubiquitin-protein ligase (E3) UBR1P |
| 73 | YMR102C | - | 4.61311719 | 11.865115 | 16.370862 | - |
| 74 | YGR177C | (ATF2) | 3.7081426 | 11.830167 | 12.555269 | Alcohol O-acetyltransferase |
| 75 | YFR034C | (PHO4) | 14.8112083 | 11.216073 | 20.844515 | Basic helix-loop-helix (BHLH) transcription factor required for expression of phosphate pathway, hyperphosphorylation by PHO80P-PHO85P cyclin-dependent protein kinase complex causes inactivation |
| 76 | YNL282W | - | 5.01708646 | 10.943286 | 13.050614 | - |
| 77 | YPL176C | - | 7.30789994 | 10.664169 | 18.424583 | Protein with similarity to SSP134P |
| 78 | YMR015C | (ERG5) | 10.2651358 | 10.313689 | 9.3557963 | Cytochrome P450 (C-22 sterol desaturase) |
| 79 | YCR061W | - | 4.07462743 | 10.291287 | 12.602668 | Protein of unknown function |
| 80 | YHL030W | (ECM29) | 4.85453872 | 10.275837 | 8.9818305 | Protein possibly involved in cell wall structure or biosynthesis |
| 81 | YPL036W | (PMA2) | 7.19300398 | 10.171951 | 12.917306 | H+-transporting P-type ATPase of the plasma membrane, expression not detected under normal growth conditions |
| 82 | YFR007W | - | 2.58144987 | 10.102403 | 6.0105766 | Protein of unknown function |
| 83 | YOL067C | (RTG1) | 30.4142081 | 10.027065 | 27.36633 | Basic helix-loop-helix (BHLH) transcription factor involved in inter-organelle communication between mitochondria, peroxisomes, and nucleus |
| 84 | YGR265W | - | 22.156977 | 9.9554618 | 5.672919 | Protein of unknown function |
| 85 | YGR293C | - | 51.4998515 | 9.7686634 | 8.066486 | Protein of unknown function |
| 86 | YMR008C | (PLB1) | 5.68517668 | 9.602215 | 11.309345 | Phospholipase B (lysophospholipase), releases fatty acids from lysophospholipids |
| 87 | YOR140W | - | 6.33829162 | 9.2015298 | 12.881145 | - |
| 88 | YML034W | - | 4.44092944 | 9.2011248 | 15.848216 | Protein of unknown function |
| 89 | YGR176W | - | 4.56487981 | 8.8866015 | 12.598661 | Protein of unknown function |
| 90 | YOR014W | (RTS1) | 7.03478812 | 8.8422619 | 11.590438 | Protein serine/threonine phosphatase 2A (PP2A), B' regulatory subunit, involved in regulation of stress-related responses and the cell cycle |
| 91 | YMR317W | - | 25.9636363 | 8.6834125 | 11.973301 | Protein of unknown function |
| 92 | YOR301W | - | 11.3702021 | 8.6327901 | 13.589223 | Protein of unknown function |
| 93 | YER119C-A | - | 8.9509545 | 8.4086333 | 6.8517264 | - |
| 94 | YOR385W | - | 6.30021483 | 8.3714543 | 10.537348 | Protein of unknown function |
| 95 | YGL156W | (AMS1) | 11.9450551 | 8.2732125 | 9.9190578 | Alpha-mannosidase, hydrolyzes terminal non-reducing alpha-D-mannose residues from alpha-D-mannosides |
| 96 | YJL219W | (HXT9) | 6.10093958 | 8.1969449 | 14.860533 | Hexose transporter, member of the sugar permease family |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 97 | YFL053W | - | 3.55404282 | 8.1217569 | 6.04425 | - |
| 98 | YNL279W | - | 2.75618909 | 8.0041323 | 12.470971 | Protein of unknown function |
| 99 | YHR007C | (ERG11) | 5.511691 | 7.8623796 | 8.6320676 | Cytochrome P450 (lanosterol 14alpha-demethylase), essential for biosynthesis of ergosterol |
| 100 | YJL127C | (SPT10) | 4.01528284 | 7.8394427 | 10.096027 | Protein that amplifies the magnitude of transcriptional regulation at various loci |
| 101 | YPL044C | - | 2.61973879 | 7.8291062 | 4.5399013 | Protein of unknown function |
| 102 | YOR030W | (DFG16) | 4.97362211 | 7.8182123 | 10.573213 | Protein involved in invasive growth upon nitrogen starvation |
| 103 | YIL011W | - | 4.59710634 | 7.3954743 | 6.7112038 | Protein with similarity to YIL176P, YIR041P and other members of the PAU1 family |
| 104 | YNR069C | - | 14.3161508 | 7.3694614 | 14.104044 | Protein of unknown function |
| 105 | YNL083W | - | 2.06305137 | 7.3050052 | 15.674556 | Protein of the mitochondrial carrier (MCF) family |
| 106 | YJL020C | - | 6.76775321 | 7.0352757 | 5.3432583 | Protein of unknown function |
| 107 | YFL065C | - | 13.5712126 | 7.0075571 | 16.704839 | Protein with similarity to other subtelomerically-encoded proteins including YHL049P, YIL177P, YJL225P, YER190P, YHR218P, and YEL076P |
| 108 | YNL329C | (PAS8) | 3.75487269 | 6.7699941 | 25.980939 | - |
| 109 | YHR006W | (STP2) | 6.44648003 | 6.5480808 | 9.270283 | Protein involved in TRNA splicing and branched-chain amino acid uptake |
| 110 | YJL221C | (FSP2) | 2.37104879 | 6.4365653 | 6.3055084 | Protein with similarity to alpha-D-glucosidase (maltase) (FSP2 and YIL172C code for identical proteins) (YIL172C and YGR287C are nearly identical) |
| 111 | YMR037C | (MSN2) | 6.80686734 | 6.4235969 | 7.6612989 | Zinc-finger transcriptional activator for genes involved in the multistress response and genes regulated through SNF1P |
| 112 | YLR379W | - | 6.34038543 | 6.4227358 | 6.8206953 | Protein of unknown function |
| 113 | YLR056W | (ERG3) | 0.03858406 | 6.2735601 | 5.191422 | C-5 sterol desaturase, an iron non-heme oxygen-requiring enzyme of the ergosterol biosynthesis pathway |
| 114 | YMR319C | (FET4) | 3.5515443 | 6.2641804 | 8.194608 | Low-affinity Fe(II) transport protein |
| 115 | YBR045C | (GIP1) | 5.88011982 | 6.254107 | 3.8135044 | GLC7P-interacting protein, possible regulatory subunit for the PP1 family protein phosphatases GLC7P |
| 116 | YKL147C | - | 4.54862611 | 6.2431328 | 10.034699 | Protein of unknown function |
| 117 | YMR135W-A | - | 15.3287997 | 6.1049555 | 4.611173 | - |
| 118 | YCR048W | (ARE1) | 9.11370518 | 6.1039374 | 10.531291 | Acyl-COA:sterol acyltransferase (sterol-ester synthetase) |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 119 | YBR235W | - | 2.65851474 | 6.1026186 | 2.9854465 | Protein with similarity to human SLC12A1 gene for which mutations are the cause of Bartter's Syndrome |
| 120 | YJL160C | - | 5.14571281 | 6.0795621 | 6.0193217 | Protein with similarity to members of the PIR1P/HSP150P/PIR3P family |
| 121 | YNL287W | (SEC21) | 5.55890054 | 6.0742978 | 5.8985117 | Coatomer complex gamma chain (gamma-COP) of secretory pathway vesicles, required for retrograde Golgi to endoplasmic reticulum transport |
| 122 | YLR458W | - | 28.2501296 | 5.9435623 | 4.6311951 | - |
| 123 | YLR121C | - | 4.04284936 | 5.9154936 | 8.131848 | - |
| 124 | YLR347C | (KAP95) | 3.84797845 | 5.8759152 | 6.4154978 | Karyopherin-beta, acts to target proteins with nuclear localization (NLS) sequences to the nuclear pore complex |
| 125 | YDL023C | - | 3.26329833 | 5.8589624 | 4.7058193 | Protein of unknown function |
| 126 | YAL010C | (MDM10) | 5.34077952 | 5.807758 | 8.9195451 | Protein involved in mitochondrial morphology and inheritance, mutant has large spherical mitochondria that do not move into the bud |
| 127 | YDR077W | (SED1) | 3.30340602 | 5.6959082 | 5.9206909 | Abundant cell surface glycoprotein, overexpression suppresses growth defect of ERD2 |
| 128 | YDR247W | - | 3.28497642 | 5.6793015 | 6.7651448 | Serine/threonine protein kinase with similarity to S. pombe RAN1 negative regulator of sexual conjugation and meiosis (GB:Z49701) |
| 129 | YBL011W | - | 3.59243122 | 5.650363 | 8.393684 | - |
| 130 | YDL025C | - | 2.91426204 | 5.5604876 | 3.9241843 | Serine/threonine protein kinase with similarity to members of the NPR1 subfamily |
| 131 | YAL013W | (DEP1) | 8.79366086 | 5.5463386 | 6.42501 | Regulator of phospholipid metabolism |
| 132 | YIL084C | (SDS3) | 1.99582364 | 5.5430688 | 6.9074225 | Suppressor of silencing defect |
| 133 | YJL213W | - | 7.09632444 | 5.4980741 | 5.5079382 | Protein with weak similarity to nocardia aryldialkylphosphatase |
| 134 | YKR053C | - | 5.37724431 | 5.4952302 | 6.4562635 | - |
| 135 | YNR042W | - | 17.7115615 | 5.4798109 | 7.5527661 | Protein of unknown function |
| 136 | YCR072C | - | 5.34712592 | 5.4565375 | 4.5985045 | Protein with similarity to nuclear MRNA processing protein PRP4P, member of WD (WD-40) repeat family |
| 137 | YER086W | (ILV1) | 4.55278717 | 5.4449008 | 4.2437712 | Serine and threonine dehydratase (anabolic), first step in isoleucine biosynthesis pathway |
| 138 | YJL076W | - | 11.4128793 | 5.4277219 | 6.6898119 | - |
| 139 | YLR072W | - | 5.19287856 | 5.4152299 | 7.2827024 | Protein of unknown function |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 140 | YDR301W | (YHH1) | 2.51614995 | 5.4121298 | 7.0975432 | - |
| 141 | YIL055C | - | 2.0005314 | 5.3410327 | 4.6542324 | Protein of unknown function |
| 142 | YEL076W-C | - | 13.2032684 | 5.3265661 | 8.0731692 | - |
| 143 | YNR047W | - | 4.44731559 | 5.3217828 | 6.1790659 | Serine/threonine protein kinase of unknown function |
| 144 | YGL211W | - | 4.00934024 | 5.2957602 | 5.5379668 | Protein of unknown function |
| 145 | YGL012W | (ERG4) | 4.57738431 | 5.2945042 | 4.833773 | Sterol C-24 reductase |
| 146 | YCL014W | (BUD3) | 2.0970839 | 5.2855114 | 3.3963317 | Protein localized at the neck filament ring required for axial budding, may provide a memory of the previous bud site |
| 147 | YBR106W | - | 5.74228482 | 5.2537051 | 9.2061479 | - |
| 148 | YHR095W | - | 5.25923706 | 5.2434619 | 2.2666062 | Protein of unknown function |
| 149 | YEL010W | - | 3.39547744 | 5.2424909 | 3.9026395 | Protein of unknown function |
| 150 | YBR005W | - | 5.58242328 | 5.2283592 | 7.5591013 | Protein of unknown function |
| 151 | YPL183C | - | 3.25331232 | 5.2150911 | 4.034456 | Protein of unknown function, has WD (WD-40) repeats |
| 152 | YJL159W | - | 5.95901062 | 5.2095163 | 5.0420867 | - |
| 153 | YBL065W | - | 5.04084137 | 5.1918263 | 10.287249 | Protein of unknown function |
| 154 | YDL071C | - | 7.24874297 | 5.1844239 | 7.5184825 | Protein of unknown function |
| 155 | YGR197C | (SNG1) | 6.43784806 | 5.17339 | 7.8870948 | Probable transport protein that confers resistance to MNNG and nitrosoguanidine |
| 156 | YLL028W | - | 9.27382002 | 5.0519624 | 5.3421753 | Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family |
| 157 | YKR034W | (DAL80) | 3.91750209 | 5.0436172 | 7.2838566 | GATA-type zinc finger transcriptional repressor for allantoin and 4-aminobutyric acid (GABA) catabolic genes |
| 158 | YDR430C | - | 2.19022255 | 5.0401778 | 3.1989703 | Protein with similarity to Class I family of aminoacyl-TRNA synthetases |
| 159 | YPL274W | - | 5.4156341 | 5.0164198 | 6.1307085 | Protein with similarity to GAP1P and other amino acid permeases |
| 160 | YMR261C | (TPS3) | 3.96385669 | 4.94376 | 3.7501015 | Component of the trehalose-6-phosphate synthase/phosphatase complex, alternate third subunit with TLS1P |
| 161 | YOL118C | - | 3.20265396 | 4.936553 | 5.7544219 | Protein of unknown function |
| 162 | YOR005C | (DNL4) | 4.47086248 | 4.8815521 | 3.6707508 | ATP-dependent DNA ligase IV, involved in non-homologous DNA end joining |
| 163 | YNL332W | - | 3.33896215 | 4.8789948 | 4.7570682 | - |
| 164 | YDR069C | (DOA4) | 3.37810593 | 4.8769723 | 5.1947947 | Ubiquitin-specific protease (ubiquitin C-terminal hydrolase) of the 26S proteasome complex, involved in vacuole biogenesis and osmoregulation |
| 165 | YOR009W | - | 59.4543494 | 4.8708102 | 5.2948993 | Protein with similarity to members of the PAU1 family |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 166 | YMR035W | (IMP2) | 9.23409301 | 4.8492871 | 5.7664813 | Inner membrane protease of mitochondria, acts in complex with IMP1P but has different substrate specificity for removal of signal peptidase |
| 167 | YER089C | (PTC2) | 2.23920866 | 4.8455014 | 5.8687657 | Protein serine/threonine phosphatase of the PP2C family |
| 168 | YJR018W | - | 5.54754057 | 4.8389334 | 4.4934937 | Protein of unknown function |
| 169 | YLR088W | (GAA1) | 3.1893544 | 4.814116 | 4.0142997 | Protein required for attachment of GPI anchor onto proteins, affects endocytosis |
| 170 | YOL163W | - | 3.92239312 | 4.8014959 | 4.5124682 | Protein with weak similarity to pseudomonas putida phthalate transporter |
| 171 | YLR462W | - | 3.32915042 | 4.7928645 | 7.1350658 | Protein of unknown function |
| 172 | YLR098C | (CHA4) | 2.05280928 | 4.7564347 | 5.5866465 | Zinc-finger protein required for activation of CHA1, has A ZN[2]-CYS[6] fungal-type binuclear cluster domain |
| 173 | YNR053C | - | 2.55991235 | 4.7234659 | 3.8186389 | Protein with similarity to human breast tumor-associated autoantigen |
| 174 | YDL246C | - | 2.43826188 | 4.6757263 | 3.5757353 | Protein with similarity to SOR1P (SOR1 and YDL246C code for nearly identical proteins) |
| 175 | YOL045W | - | 3.55662236 | 4.672513 | 2.0538279 | Serine/threonine protein kinase of unknown function |
| 176 | YKL176C | - | 3.32695888 | 4.6429893 | 5.4538239 | Protein of unknown function |
| 177 | YJR114W | - | 3.00664482 | 4.6389866 | 4.0045917 | Protein of unknown function |
| 178 | YER091C | (MET6) | 6.67067887 | 4.6224571 | 2.9292597 | Homocysteine methyltransferase (5-methyltetrahydropteroyl triglutamate--homocysteine methyltransferase), methionine synthase, cobalamin-independent |
| 179 | YHL049C | - | 5.15537247 | 4.5637645 | 9.5066446 | Protein with similarity to other subtelomerically-encoded proteins including YER189P, YML133P, and YJL225P, coded from a subtelomeric Y' region |
| 180 | YDR389W | (SAC7) | 3.89197011 | 4.5609599 | 4.3143109 | GTPase-activating protein for RHO1P |
| 181 | YMR202W | (ERG2) | 9.58572292 | 4.5446614 | 5.575174 | Sterol C8-C7 isomerase (C-8 sterol isomerase), enzyme of the ergosterol biosynthesis pathway |
| 182 | YBL019W | - | 3.45990928 | 4.4694518 | 4.1655454 | - |
| 183 | YGR287C | - | 10.2933872 | 4.4595137 | 9.7718104 | Protein with similarity to alpha-D-glucosidase (maltase) (YGR287C IS nearly identical to FSP2 and YIL172C) |
| 184 | YJL082W | - | 7.42175571 | 4.4522595 | 5.556901 | Protein of unknown function |
| 185 | YHR098C | - | 2.51284975 | 4.4353768 | 4.3716652 | Protein of unknown function |
| 186 | YOR371C | - | 2.47743776 | 4.4289864 | 5.2783501 | Protein of unknown function |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 187 | YDR530C | (APA2) | 2.40849553 | 4.3993312 | 2.7389073 | ATP adenylyltransferase II (AP4A phosphorylase) |
| 188 | YKL119C | (VPH2) | 0.16462534 | 4.3613346 | 0 | Vacuolar H-ATPase (V-ATPase) assembly protein acting in the endoplasmic reticulum |
| 189 | YOR273C | - | 13.0544715 | 4.3469302 | 10.649131 | Protein with similarity to members of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family |
| 190 | YPL042C | (SSN3) | 6.78272968 | 4.3344728 | 3.9578568 | Cyclin-dependent serine/threonine protein kinase of the RNA polymerase II holoenzyme complex and Kornberg's mediator (SRB) subcomplex |
| 191 | YGR268C | - | 4.77373538 | 4.3329069 | 5.2744105 | Protein of unknown function |
| 192 | YPR011C | - | 2.0077462 | 4.3123349 | 4.2742986 | Protein with similarity to human Grave's Disease carrier protein (SP:P16260) and to bovine homolog of Grave's Disease carrier protein (SP:Q01888) |
| 193 | YPL022W | (RAD1) | 4.48327554 | 4.3036056 | 6.5285426 | Component of the nucleotide excision repairosome, homolog of human XPF xeroderma pigmentosum gene product and the mammalian ERCC-4 protein |
| 194 | YGL207W | (SPT16) | 5.34289635 | 4.3033021 | 3.5727713 | General chromatin factor required for adequate expression of CLN and other genes |
| 195 | YGL167C | (PMR1) | 4.12359747 | 4.2628564 | 4.8141347 | CA++-transporting P-type ATPase of Golgi membrane involved in CA++ import into Golgi |
| 196 | YJR091C | (JSN1) | 4.56429439 | 4.2419881 | 4.7804157 | Protein that when overexpressed can suppress the hyperstable microtubule phenotype of TUB2-150 |
| 197 | YDR238C | (SEC26) | 4.48641405 | 4.2179222 | 3.8109695 | Coatomer complex beta chain (beta-COP) of secretory pathway vesicles, required for retrograde transport from Golgi to endoplasmic reticulum |
| 198 | YDL012C | - | 2.90930997 | 4.2158147 | 2.0519798 | Protein of unknown function |
| 199 | YDR044W | (HEM13) | 14.9283272 | 4.2136787 | 3.4946018 | Coproporphyrinogen III oxidase, oxygen-repressed, sixth step in heme-biosynthetic pathway |
| 200 | YGL114W | - | 3.22707938 | 4.2023503 | 5.0073787 | Protein with similarity to S. pombe ISP4 protein, member of the major facilitator superfamily (MFS) |
| 201 | YGL055W | (OLE1) | 2.29875509 | 4.1923045 | 3.5992372 | Stearoyl-COA desaturase (delta-9 fatty acid desaturase), required for synthesis of unsaturated fatty acids |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 202 | YDL088C | (ASM4) | 4.39685251 | 4.1757265 | 3.321034 | Suppressor of temperature-sensitive mutations in POL3P (DNA polymerase delta) |
| 203 | YKL171W | - | 2.64137608 | 4.1581147 | 8.2933538 | Serine/threonine protein kinase of unknown function |
| 204 | YPL190C | - | 5.94196213 | 4.1575162 | 3.202837 | - |
| 205 | YMR140W | - | 5.24432896 | 4.157179 | 5.4545409 | Protein of unknown function |
| 206 | YBL005W | (PDR3) | 3.75060207 | 4.1449054 | 6.0827305 | Transcription factor related to PDR1P, contains a ZN[2]-CYS[6] fungal-type binuclear cluster domain in the N-terminal region |
| 207 | YML032C | (RAD52) | 3.13968668 | 4.1330793 | 3.0832115 | Protein required for recombination and repair of X-ray damage, has a late function in meiotic recombination |
| 208 | YFR018C | - | 5.28886874 | 4.1041589 | 6.4001917 | Protein with similarity to human glutaminyl-peptide cyclotransferase |
| 209 | YGL125W | (MET11) | 6.80542292 | 4.0762178 | 4.4382484 | - |
| 210 | YCR057C | (PWP2) | 3.34704165 | 4.0555292 | 3.4118145 | - |
| 211 | YBL044W | - | 4.67885642 | 4.0526493 | 9.1998322 | Protein of unknown function |
| 212 | YPL268W | (PLC1) | 2.90633764 | 4.0372127 | 2.1993847 | Phosphoinositide-specific phospholipase C (1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase 1), produces diacylglycerol and inositol 1,4,5-trisphosphate |
| 213 | YOR204W | (DED1) | 2.52920945 | 4.0291663 | 3.0830731 | ATP-dependent RNA helicase of dead box family involved in protein synthesis |
| 214 | YPL171C | (OYE3) | 4.94122983 | 4.0225239 | 0.2747214 | NAPDH dehydrogenase (old yellow enzyme), isoform 3 |
| 215 | YOR203W | - | 3.473713 | 3.9900922 | 3.2232019 | Protein of unknown function |
| 216 | YNL295W | - | 2.855052 | 3.9889367 | 2.1389666 | Protein of unknown function |
| 217 | YEL042W | (GDA1) | 2.00067395 | 3.9856733 | 3.8058139 | Guanosine diphosphatase of Golgi membrane |
| 218 | YLR339C | - | 4.12619065 | 3.9844972 | 3.506939 | Protein of unknown function |
| 219 | YIL007C | - | 5.11957134 | 3.9770005 | 2.318674 | Protein of unknown function |
| 220 | YIR007W | - | 3.71972069 | 3.9670484 | 5.0861072 | Protein with similarity to endoglucanase |
| 221 | YER114C | (BOI2) | 2.5967273 | 3.9643546 | 6.3042836 | Protein with SH3 domain involved in bud formation, binds to BEM1P |
| 222 | YLR092W | (SUL2) | 6.02237117 | 3.9547891 | 4.5438793 | High-affinity sulfate transporter |
| 223 | YEL060C | (PRB1) | 5.60961951 | 3.939317 | 4.7370327 | Protease B (YSCB) (PRB) (cerevisin), serine protease of the subtilisin family with broad proteolytic specificity |
| 224 | YAL051W | - | 2.40553928 | 3.9334781 | 4.5099518 | - |
| 225 | YJR147W | - | 2.05911726 | 3.9267937 | 5.1956856 | - |
| 226 | YOR386W | (PHR1) | 1.99823774 | 3.9204076 | 5.7096569 | Deoxyribodipyrimidine photolyase, involved in light-dependent repair of pyrimidine dimers |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 227 | YCR037C | (PHO87) | 2.81200613 | 3.8982171 | 4.0311884 | Member of the phosphate permease family of the major facilitator superfamily |
| 228 | YOL100W | - | 3.04632994 | 3.8854218 | 9.2592192 | Serine/threonine protein kinase of unknown function |
| 229 | YBL047C | - | 3.40597241 | 3.88363 | 5.2814809 | Protein with similarity to cytoskeletal protein USO1P, PAN1P, and mouse tyrosine kinase substrate EPS15 |
| 230 | YAR014C | - | 2.53512963 | 3.823947 | 4.4065791 | Protein of unknown function |
| 231 | YKL182W | (FAS1) | 3.75368336 | 3.8068781 | 5.3493259 | Fatty-acyl-COA synthase, beta chain (contains acetyl transferase, enoyl reductase, dehydratase, and malonyl/palmitoyl transferase) |
| 232 | YLR331C | - | 3.94099666 | 3.795387 | 3.3715843 | Protein of unknown function |
| 233 | YEL031W | (SPF1) | 7.77512435 | 3.7891074 | 4.357615 | Protein with similarity to CA++-transporting ATPases |
| 234 | YHR078W | - | 2.2941334 | 3.7838221 | 4.6151917 | Protein of unknown function, has 4 potential transmembrane domains |
| 235 | YPL155C | (KIP2) | 3.29502679 | 3.7807978 | 9.392792 | Kinesin-related protein |
| 236 | YNR074C | - | 4.3061075 | 3.7638306 | 5.7991531 | Protein with similarity to Bacillus subtilis nitrite reductase (NIRB) |
| 237 | YMR303C | (ADH2) | 4.56919214 | 3.7542967 | 3.1957867 | Alcohol dehydrogenase II, glucose-repressed |
| 238 | YLR134W | (PDC5) | 4.9450653 | 3.7528169 | 3.2704832 | Pyruvate decarboxylase isozyme 2 |
| 239 | YKL067W | (YNK1) | 4.49102455 | 3.7325797 | 3.6497934 | Nucleoside diphosphate kinase, responsible for synthesis of all nucleoside triphosphates except ATP |
| 240 | YLR136C | (TIS11) | 2.88004451 | 3.7255421 | 5.1711798 | - |
| 241 | YDR443C | (SCA1) | 2.75733315 | 3.7068432 | 6.9331513 | - |
| 242 | YGL071W | (RCS1) | 3.39203358 | 3.6963077 | 4.5310166 | Regulatory protein involved in IRON uptake |
| 243 | YBR293W | - | 2.25740646 | 3.6840827 | 3.0384171 | Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family |
| 244 | YMR324C | - | 3.33053542 | 3.6802526 | 2.8779503 | Protein with similarity to members of the YBL108P/YCR103P/ YKL223P family |
| 245 | YFL051C | - | 2.07690974 | 3.6611179 | 4.7476201 | Protein with similarity to FLO1P family of proteins |
| 246 | YBR276C | (PPS1) | 2.35950244 | 3.6550406 | 3.4539593 | Protein tyrosine phosphatase (PTPase) with dual specificity |
| 247 | YFL042C | - | 3.57726533 | 3.6509118 | 4.5694594 | Protein of unknown function, has similarity to YHR080P |
| 248 | YPL263C | (KEL3) | 4.50871509 | 3.6484792 | 3.8498382 | Protein with similarity to KEL1P and KEL2P |
| 249 | YLR188W | (MDL1) | 5.00498919 | 3.6478982 | 4.3936321 | ATP-binding cassette (ABC) superfamily member, equivalent to a "half-molecule" ABC protein plus an ATP-binding domain |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 250 | YPR021C | - | 2.21061647 | 3.6466639 | 3.2312479 | Protein with similarity to proteins of the mitochondrial carrier (MCF) family (GB:Z49274) |
| 251 | YKL138C | (MRPL31) | 3.22538649 | 3.6454084 | 4.0488722 | Mitochondrial ribosomal protein of the large subunit (YML31) |
| 252 | YNL148C | (ALF1) | 3.33997835 | 3.6391378 | 5.2515594 | Alpha-tubulin foldin, cofactor B |
| 253 | YLR302C | - | 10.5636377 | 3.6318383 | 0.3621924 | Protein of unknown function |
| 254 | YBR298C | (MAL31) | 5.44502575 | 3.6302693 | 9.8311328 | High affinity maltoaseH+ symporter (maltose permease) member of the sugar permease family |
| 255 | YAR044W | (OSH1) | 4.12112011 | 3.624939 | 3.8839622 | Protein implicated in ergosterol biosynthesis, member of the KES1/HES1/OSH1/YKR003W family of oxysterol-binding (OSBP) proteins |
| 256 | YLR120C | (YAP3) | 6.14265883 | 3.6229845 | 4.4298562 | Transcription factor of the basic leucine zipper (BZIP) family, one of eight members of a novel fungal-specific family of BZIP proteins |
| 257 | YGR134W | - | 2.8756723 | 3.6189405 | 1.9505784 | Protein of unknown function |
| 258 | YMR088C | - | 3.01763425 | 3.574571 | 2.5742717 | Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family 2 |
| 259 | YDR291W | - | 4.95353348 | 3.5637613 | 2.8803997 | Protein with similarity to SGS1P and other DNA helicases |
| 260 | YJR017C | (ESS1) | 2.98118086 | 3.5587415 | 3.2208256 | Processing/termination factor, involved in transcription termination or 3'-end processing of pre-MRNA |
| 261 | YGL178W | (MPT5) | 4.28561965 | 3.558276 | 3.3338238 | Protein required for high temperature growth, recovery from alpha-factor arrest, and normal lifespan of yeast cells |
| 262 | YHR086W | (NAM8) | 2.63503306 | 3.556686 | 4.1441189 | U1 SNRNA-associated protein, essential for meiotic recombination and suppressor of mitochondrial splicing defects, has 3 RNA recognition (RRM) domains poly(A)-binding protein |
| 263 | YGR178C | (PBP1) | 2.95926792 | 3.5559294 | 3.6095103 | |
| 264 | YBL022C | (PIM1) | 4.1993836 | 3.5255118 | 3.2518435 | Serine protease required for intramitochondrial proteolysis and maintenance of respiratory function, related to E. coli ATP-dependent protease LA |
| 265 | YJL083W | - | 3.34026267 | 3.5131828 | 5.6812601 | Protein with similarity to IRS4P |
| 266 | YJR053W | - | 2.12253894 | 3.5096202 | 4.5401439 | Protein involved in efficiency of mating |
| 267 | YJL175W | - | 6.11781731 | 3.5040684 | 3.7938536 | Protein of unknown function |
| 268 | YMR016C | - | 3.67893179 | 3.4720987 | 3.3111279 | - |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 269 | YLL051C | (FRE6) | 2.59520796 | 3.4643555 | 4.4566151 | Protein with similarity to ferric reductase FRE2P |
| 270 | YJL212C | - | 4.42206996 | 3.458335 | 4.0764022 | Protein with similarity to S. pombe ISP4+ which is induced by sexual differentiation |
| 271 | YMR019W | (STB4) | 3.2576922 | 3.4414621 | 3.397646 | SIN3P-binding protein, has ZN[2]-CYS[6] fungal-type binuclear cluster domain in the N-terminal region |
| 272 | YHL047C | - | 3.02606918 | 3.4089434 | 3.007693 | Member of major facilitator superfamily (MFS) multidrug-resistance (MFS-MDR) protein family |
| 273 | YBR038W | (CHS2) | 2.03060756 | 3.3885338 | 2.8509884 | Chitin synthase II, responsible for primary septum disk |
| 274 | YLR023C | - | 2.68880866 | 3.3876183 | 2.5555381 | Protein of unknown function |
| 275 | YPL009C | - | 5.28314415 | 3.3856037 | 0.8412905 | Protein of unknown function |
| 276 | YGL008C | (PMA1) | 2.09210526 | 3.3844005 | 3.725269 | H+-transporting P-type ATPase of the plasma membrane, activity is rate-limiting for growth at low pH |
| 277 | YMR033W | (ARP9) | 3.08586194 | 3.3800103 | 2.9005564 | Protein with similarity to actin and actin-related proteins ARP1P-ARP10P |
| 278 | YLR153C | (ACS2) | 3.45528019 | 3.3785446 | 3.1285812 | Acetyl-COA synthetase (acetate-COA ligase) |
| 279 | YLL061W | - | 10.9366799 | 3.369477 | 3.0795633 | Protein with similarity to GAP1P and other amino acid permeases |
| 280 | YNL192W | (CHS1) | 3.72575719 | 3.358192 | 3.7457248 | Chitin synthase I, has a repair function during cell separation |
| 281 | YEL058W | (PCM1) | 4.56623631 | 3.3482618 | 3.4456437 | Hexosephosphate mutase (phosphoacetylglucosamine mutase) (N-acetylglucosamine-phosphate mutase), converts N-acetyl-D-glucosamine 1-phosphate to N-acetyl-D-glucosamine 6-phosphate |
| 282 | YLR099C | - | 4.72209646 | 3.3290462 | 2.9774757 | Protein of unknown function |
| 283 | YDL057W | - | 3.21787484 | 3.316811 | 4.4492894 | Protein of unknown function |
| 284 | YLR195C | (NMT1) | 3.4535546 | 3.3142347 | 3.1727409 | N-myristoyltransferase, adds myristoyl group to N-terminal glycine of certain proteins |
| 285 | YAL005C | (SSA1) | 3.48582964 | 3.3068323 | 2.9388227 | Heat shock protein of HSP70 family, cytoplasmic |
| 286 | YPL222W | - | 2.79485782 | 3.2974442 | 2.9997551 | Protein of unknown function |
| 287 | YJL056C | - | 2.36206747 | 3.2790296 | 3.3129634 | - |
| 288 | YKR021W | - | 2.33705924 | 3.269552 | 2.936447 | Protein of unknown function |
| 289 | YPL119C | (DBP1) | 5.87199247 | 3.2464223 | 2.197366 | ATP-dependent RNA helicase of dead box family, suppressor of SPP81/DED1 |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 290 | YGL014W | - | 3.11296478 | 3.2294295 | 3.6382821 | Protein with pumilio repeats that is involved with MPT5P in relocalization of SIR3P and SIR4P from telomeres to the nucleolus |
| 291 | YER010C | - | 11.4713039 | 3.2179542 | 2.3807886 | Protein of unknown function |
| 292 | YJR151C | - | 41.4229667 | 3.2130608 | 4.5216913 | Protein of unknown function |
| 293 | YPL207W | - | 2.48831068 | 3.2080219 | 2.9864022 | Protein of unknown function |
| 294 | YER130C | - | 2.01652303 | 3.2075344 | 3.3332725 | Protein of unknown function |
| 295 | YNR065C | - | 2.86361451 | 3.2060768 | 7.3945002 | Protein with similarity to PEP1P |
| 296 | YGL192W | (IME4) | 2.89030953 | 3.170381 | 6.4784105 | Positive transcription factor for IME1 and IME2, mediates control of meiosis by carrying signals regarding mating type (A/alpha) and nutritional status |
| 297 | YMR047C | (NUP116) | 2.56622055 | 3.1702234 | 4.7742052 | Nuclear pore protein (nucleoporin) of the GLFG family, may be involved in binding and translocation of nuclear proteins |
| 298 | YDR256C | (CTA1) | 4.54027942 | 3.158248 | 8.0093186 | Catalase A (peroxisomal) |
| 299 | YDR208W | (MSS4) | 2.61164524 | 3.154316 | 3.0423151 | Potential PI P 5-kinase, multicopy suppressor of STT4 mutation |
| 300 | YHR214W | - | 4.54013428 | 3.1513793 | 5.6325011 | Protein of unknown function (YAR066W and YHR214W code for identical proteins) |
| 301 | YLR249W | (YEF3) | 3.59397167 | 3.1445334 | 2.631954 | Translation elongation factor EF-3A, member of ATP-binding cassette (ABC) superfamily |
| 302 | YNL331C | - | 3.44801501 | 3.1185277 | 6.5303136 | Probable aryl-alcohol reductase |
| 303 | YPR115W | - | 2.4843458 | 3.1174643 | 2.5667848 | Protein of unknown function |
| 304 | YJL178C | - | 2.60257256 | 3.1121969 | 2.7705734 | Protein of unknown function |
| 305 | YAR042W | (SWH1) | 18.1940127 | 3.0992362 | 6.2488302 | Protein of unknown function |
| 306 | YDR015C | - | 0.09079169 | 3.0861607 | 0.3097629 | Protein of unknown function |
| 307 | YBL067C | (UBP13) | 3.41427731 | 3.0820393 | 2.4717411 | Ubiquitin C-terminal hydrolase |
| 308 | YHR072W | (ERG7) | 3.5569619 | 3.0809956 | 3.4311189 | Lanosterol synthase, carries out complex cyclization step of squalene to lanosterol in ergosterol biosynthesis pathway |
| 309 | YAL028W | - | 9.17485562 | 3.0726043 | 3.8109858 | Protein of unknown function |
| 310 | YIR015W | - | 2.80351347 | 3.066482 | 3.4328314 | Subunit of RNase P |
| 311 | YMR308C | (PSE1) | 2.69422447 | 3.0659484 | 2.6409014 | - |
| 312 | YOR345C | - | 5.73841888 | 3.0523183 | 2.2898958 | Deoxycytidyl transferase involved in mutagenic translesion DNA synthesis |
| 313 | YPL193W | - | 3.60415592 | 3.0500696 | 2.8450987 | Protein of unknown function |
| 314 | YFR012W | - | 3.31259823 | 3.0316711 | 0 | Protein of unknown function |
| 315 | YPL205C | - | 13.258257 | 3.0208358 | 0.7999155 | Protein of unknown function |
| 316 | YDR476C | - | 8.1273943 | 3.0155987 | 3.8636781 | Protein of unknown function |
| 317 | YCR052W | (RSC6) | 2.2744649 | 3.0112438 | 2.6017436 | Component of abundant chromatin remodeling complex (RSC) |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 318 | YGL022W | (STT3) | 3.64275733 | 3.0050118 | 3.8854905 | Oligosaccharyltransferase subunit, member of a complex of eight ER proteins that transfers core oligosaccharide from dolichol carrier to Asn-X-Ser/Thr motif |
| 319 | YMR109W | - | 19.0544656 | 3.0044499 | 5.6886658 | - |
| 320 | YHR032W | - | 9.30722933 | 2.9855823 | 4.5560581 | Protein of unknown function, member of the major facilitator superfamily(MFS) |
| 321 | YLR236C | - | 2.6190617 | 2.9810987 | 3.7681402 | - |
| 322 | YOR337W | (TEA1) | 2.13152473 | 2.9790715 | 4.8228581 | TY1 enhancer activator of the GAL4P-type family of DNA-binding proteins |
| 323 | YFR055W | - | 2.35867872 | 2.9771983 | 3.0622139 | Protein with similarity to E. coli cystathionine beta-lyase |
| 324 | YHR212C | - | 4.01639255 | 2.9769438 | 4.4451423 | Protein identical to YAR060P/RAA19P |
| 325 | YLR001C | - | 2.77031036 | 2.9663037 | 2.7628132 | Protein of unknown function |
| 326 | YOR034C | - | 3.38439363 | 2.9543526 | 2.5499862 | - |
| 327 | YPR076W | - | 3.86182393 | 2.9410933 | 3.2728075 | Protein of unknown function |
| 328 | YKL183W | - | 2.9718977 | 2.9334031 | 5.2561547 | Protein of unknown function |
| 329 | YBR004C | - | 3.05485559 | 2.9257736 | 2.8905869 | Protein expressed between 3 and 6 hours after transfer to sporulation medium |
| 330 | YJR071W | - | 3.39019477 | 2.924417 | 1.768982 | Protein of unknown function |
| 331 | YCR084C | (TUP1) | 2.40138822 | 2.9219843 | 3.2718264 | General repressor of transcription (with SSN6P), member of WD (WD-40) repeat family |
| 332 | YFR030W | (MET10) | 33.6060485 | 2.9138815 | 2.0879079 | Assimilatory sulfite reductase subunit, flavin-binding (alpha) subunit, part of the sulfate assimilation pathway |
| 333 | YKL148C | (SDH1) | 2.72554507 | 2.9036242 | 2.5317298 | Succinate dehydrogenase (ubiquinone) flavoprotein (FP) subunit, converts succinate + ubiquinone to fumarate + ubiquinol in the TCA cycle |
| 334 | YER044C | - | 3.6669641 | 2.9002716 | 2.6807728 | Protein of unknown function |
| 335 | YLR045C | (STU2) | 2.16969039 | 2.8946579 | 2.9923107 | Component of the spindle pole body |
| 336 | YPL226W | - | 2.45263084 | 2.8885678 | 2.5557944 | Protein with similarity to members of the ATP-binding cassette (ABC) superfamily |
| 337 | YHR161C | - | 2.86345744 | 2.8873374 | 2.9469349 | - |
| 338 | YJR109C | (CPA2) | 4.31426739 | 2.8803515 | 3.1263529 | Carbamoylphosphate synthase (glutamine-hydrolyzing) arginine-specific, large chain |
| 339 | YGR250C | - | 2.20914388 | 2.8752914 | 3.8774955 | Protein of unknown function, has three RNA recognition (RRM) domains |
| 340 | YLR149C | - | 3.39994503 | 2.8694003 | 4.6627573 | Protein of unknown function |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 341 | YCL057W | (PRD1) | 3.49569406 | 2.8641379 | 2.7495149 | Proteinase YSCD, saccharolysin, contains zinc metalloendoprotease motif HEXXH |
| 342 | YLR114C | - | 2.27233205 | 2.8496505 | 1.8650501 | Protein with weak similarity in the C-terminus to drosophila melanogaster bicaudal-D protein |
| 343 | YML075C | (HMG1) | 2.71708812 | 2.8491957 | 3.2059005 | 3-hydroxy-3-methylglutaryl-coenzyme A reductase 1, rate limiting enzyme for sterol biosynthesis, converts HMG-COA to mevalonate |
| 344 | YLR397C | (AFG2) | 2.56801854 | 2.8469125 | 2.7385515 | Protein of the AAA family of ATPases, has similarity to mammalian valosin-containing protein (VCP) |
| 345 | YJR019C | (TES1) | 4.07777555 | 2.8303235 | 2.0724897 | Acyl-COA thioesterase |
| 346 | YBL008W | (HIR1) | 7.24580603 | 2.8284713 | 2.8866813 | Histone transcription inhibitor, required for periodic repression of 3 of the 4 histone gene loci and for autogenous repression of HTA1-HTB1 locus by H2A and H2B |
| 347 | YGL062W | (PYC1) | 2.649771 | 2.8279558 | 3.1059191 | Pyruvate carboxylase 1, converts pyruvate to oxaloacetate for gluconeogenesis |
| 348 | YPL244C | - | 3.43385233 | 2.8218119 | 3.3274479 | Protein of unknown function |
| 349 | YGL001C | - | 3.91981575 | 2.8214816 | 1.9852785 | Protein with similarity to nocardia SP. cholesterol dehydrogenase |
| 350 | YMR302C | (PRP12) | 2.92335545 | 2.8146501 | 2.7190981 | - |
| 351 | YPL160W | (CDC60) | 2.25327101 | 2.8142723 | 1.7426948 | Leucyl-TRNA synthetase, cytoplasmic |
| 352 | YLL024C | (SSA2) | 4.09160949 | 2.8142088 | 2.4784071 | Heat shock protein of HSP70 family, cytoplasmic |
| 353 | YEL077C | - | 3.20718793 | 2.8098429 | 3.9054119 | - |
| 354 | YMR205C | (PFK2) | 2.27470363 | 2.8050429 | 2.2843952 | Phosphofructokinase beta subunit, part of a complex with PFK1P which carries out key regulatory step in glycolysis |
| 355 | YPL114W | - | 4.16484234 | 2.7962162 | 1.717967 | Protein of unknown function |
| 356 | YPL221W | - | 4.08515832 | 2.7886642 | 3.960997 | Protein of unknown function |
| 357 | YJR137C | (ECM17) | 26.5435466 | 2.787597 | 2.0763181 | Putative sulfite reductase (ferredoxin) |
| 358 | YKL164C | (PIR1) | 2.11125363 | 2.7864791 | 2.3925674 | Protein required for tolerance to heat shock, member of the PIR1P/HSP150P/PIR3P family |
| 359 | YCL037C | (SRO9) | 8.35007693 | 2.7855748 | 2.393588 | Suppressor of YPT6 null and RHO3 mutations |
| 360 | YHR082C | (KSP1) | 2.14499054 | 2.7799591 | 3.4962633 | Serine/threonine kinase that suppresses PRP20 mutant when overproduced |
| 361 | YPR074C | - | 3.19760669 | 2.7711859 | 2.476508 | - |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 362 | YBR184W | (MEL1) | 5.06354303 | 2.7711448 | 3.5340388 | Alpha-galactosidase (melibiase), converts melibiose into galactose + glucose, converts melibiose to galactose and glucose |
| 363 | YOL157C | - | 2.70064964 | 2.7668777 | 3.6204284 | Probable alpha-glucosidase |
| 364 | YFL066C | - | 2.94443276 | 2.753026 | 3.5848427 | Protein with similarity to other subtelomerically-encoded proteins including YIL177P, YHL050P, and YER190P |
| 365 | YLL029W | - | 2.22657399 | 2.7389102 | 3.1468025 | Protein of unknown function |
| 366 | YJL198W | - | 2.98124683 | 2.7343513 | 4.6395823 | Protein with strong similarity to PHO87P, member of the phosphate permease family of the major facilitator superfamily (MFS) |
| 367 | YDR088C | (SLU7) | 2.07293165 | 2.7339627 | 2.6876744 | Pre-MRNA splicing factor affecting 3' splice site choice, required only for the second catalytic step of splicing |
| 368 | YJR132W | (NMD5) | 3.2005363 | 2.7333821 | 3.208398 | Member of the karyopherin-beta family, possibly involved in nuclear transport |
| 369 | YIL078W | (THS1) | 3.31778832 | 2.7330794 | 1.6123939 | Threonyl-TRNA synthetase, cytoplasmic, member of Class II family of aminoacyl-TRNA synthetases |
| 370 | YGL113W | - | 2.33404789 | 2.7249323 | 3.3810122 | Protein of unknown function |
| 371 | YMR086W | - | 2.69384376 | 2.7191747 | 2.9840404 | Protein of unknown function |
| 372 | YGL233W | (SEC15) | 2.61433498 | 2.7141295 | 2.7961427 | Component of exocyst complex required for exocytosis |
| 373 | YGL144C | - | 2.26752066 | 2.7069494 | 2.6236889 | Protein of unknown function |
| 374 | YOR137C | - | 3.14249753 | 2.7031211 | 4.9526236 | Protein of unknown function |
| 375 | YJR143C | (PMT4) | 2.80130312 | 2.6954799 | 2.4879264 | Mannosyltransferase (dolichyl phosphate-D-mannose:protein O-D-mannosyltransferase), involved in initiation of O-glycosylation |
| 376 | YBR289W | (SNF5) | 2.00671327 | 2.6881295 | 3.038619 | Component of SWI/SNF global transcription activator complex, acts to assist gene-specific activators through chromatin remodeling |
| 377 | YNL240C | - | 5.13894557 | 2.685901 | 3.523963 | Protein with similarity to kluyveromyces MARX. LET1 protein |
| 378 | YML013W | - | 3.62672833 | 2.6831604 | 2.9292996 | Protein of unknown function |
| 379 | YKL168C | - | 2.43589311 | 2.6791837 | 3.1896257 | - |
| 380 | YGL151W | (NUT1) | 2.47823061 | 2.6787971 | 2.5683618 | Protein that affects expression of HO |
| 381 | YNL197C | (WHI3) | 2.51493336 | 2.6764555 | 3.4233233 | Protein involved in regulation of cell size, has 1 RNA recognition (RRM) domain |
| 382 | YMR192W | - | 2.18376269 | 2.6732126 | 2.7489187 | Protein with similarity to mouse TBC1 protein |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 383 | YAL038W | (CDC19) | 2.63679951 | 2.6714535 | 2.7525692 | - |
| 384 | YEL075C | - | 5.12225893 | 2.6632638 | 3.778537 | Protein with similarity to other subtelomerically-encoded proteins including YHL049P, YIL177P, and YJL225P |
| 385 | YHR219W | - | 3.76398139 | 2.6619567 | 4.0207342 | Protein with similarity to other subtelomerically-encoded proteins |
| 386 | YJL069C | - | 2.65731007 | 2.6517254 | 2.6568606 | Protein of unknown function |
| 387 | YLR125W | - | 6.28348756 | 2.642933 | 3.1335402 | Protein of unknown function |
| 388 | YML035C | (AMD1) | 2.23864371 | 2.6401405 | 1.6690608 | AMP deaminase, converts AMP to IMP and ammonia |
| 389 | YMR165C | (SMP2) | 2.58642399 | 2.6310411 | 3.3572604 | Protein whose deletion causes increased plasmid stability |
| 390 | YDL223C | - | 3.16684859 | 2.6240147 | 2.2340877 | Protein of unknown function |
| 391 | YLR138W | - | 2.69090586 | 2.6158483 | 2.9821754 | - |
| 392 | YAR020C | - | 3.79173888 | 2.6111125 | 2.0234222 | - |
| 393 | YLR337C | (VRP1) | 6.57336326 | 2.6027011 | 3.7504037 | Proline-rich protein verprolin, involved in cytoskeletal organization and cellular growth |
| 394 | YLR060W | (FRS1) | 2.61550639 | 2.5992071 | 1.9335426 | Phenylalanyl-TRNA synthetase, alpha subunit, cytoplasmic |
| 395 | YLL013C | - | 2.93447915 | 2.5901954 | 4.1297767 | Protein with similarity to drosophila pumilio protein |
| 396 | YIR003W | - | 2.41363594 | 2.5863745 | 2.874494 | Protein with similarity to E. coli and Bacillus subtilis mind, has potential coiled-coil region |
| 397 | YIL137C | - | 2.27968603 | 2.5792356 | 1.9624104 | Protein with similarity to aminopeptidases |
| 398 | YBL081W | - | 2.34404421 | 2.573205 | 3.2079939 | Protein with 37% identity to drosophila L not protein |
| 399 | YOR171C | - | 3.59659097 | 2.5718305 | 2.4035974 | - |
| 400 | YPL237W | (SUI3) | 2.5966981 | 2.5628077 | 2.5479456 | Translation initiation factor EIF2beta subunit |
| 401 | YHR142W | - | 3.52383057 | 2.5597096 | 2.9887896 | Protein of unknown function |
| 402 | YLL012W | - | 3.25020683 | 2.550591 | 2.7451737 | Protein with similarity to human triacylglycerol lipase |
| 403 | YFR025C | (HIS2) | 2.5112362 | 2.5457991 | 2.8789156 | Histidinol phosphatase |
| 404 | YGR240C | (PFK1) | 2.24103063 | 2.5388997 | 2.4938739 | Phosphofructokinase alpha subunit, part of a complex with PFK2P which carries out A key regulatory step in glycolysis |
| 405 | YPL101W | - | 4.18961695 | 2.5351198 | 2.6201803 | Protein of unknown function |
| 406 | YOR127W | (RGA1) | 3.85804733 | 2.5316649 | 2.5697341 | RHO-type GTPase-activating protein (GAP) for CDC42P |
| 407 | YBR088C | (POL30) | 2.5383718 | 2.5276319 | 4.0628861 | Proliferating cell nuclear antigen (PCNA), required for DNA synthesis and DNA repair |
| 408 | YBR295W | (PCA1) | 4.16669535 | 2.525791 | 1.1221384 | P-type copper-transporting ATPase |
| 409 | YCL044C | - | 2.35958836 | 2.519608 | 3.263571 | Protein of unknown function |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 410 | YBR110W | (ALG1) | 2.23384099 | 2.5141215 | 3.2250999 | Beta-mannosyltransferase involved in N-glycosylation (transfers MAN from GDP-MAN to DOL-PP-GLCNAC2) |
| 411 | YGR175C | (ERG1) | 6.02726287 | 2.5103577 | 1.8132661 | Squalene monooxygenase (squalene epoxidase), enzyme of the ergosterol biosynthesis pathway |
| 412 | YLR116W | - | 2.98116702 | 2.5079761 | 3.9707409 | - |
| 413 | YCR068W | - | 3.32107678 | 2.4920381 | 3.6811994 | Protein of unknown function |
| 414 | YJR105W | - | 2.20476096 | 2.4908887 | 1.7029385 | Protein with similarity to ribokinase |
| 415 | YKL157W | (APE2) | 2.18209838 | 2.4866194 | 2.093134 | Aminopeptidase II (YSCII), plays a nutritional role in releasing leucine from peptides externally cleaved at leucine |
| 416 | YFR009W | (GCN20) | 2.63782118 | 2.4859544 | 2.1613378 | Component of a protein complex required for activation of GCN2P protein kinase in response to amino acid starvation, member of ATP-binding cassette (ABC) superfamily |
| 417 | YDR211W | (GCD6) | 2.22567451 | 2.4835485 | 1.8240639 | Translation initiation factor EIF2B (guanine nucleotide exchange factor), 81 KDA (beta) subunit |
| 418 | YAR060C | - | 4.88485967 | 2.482682 | 4.6114571 | Protein identical to YHR212P, has a predicted mitochondrial transit peptide |
| 419 | YJL187C | (SWE1) | 2.01161328 | 2.4809757 | 2.6294797 | Serine/tyrosine dual-specificity protein kinase able to phosphorylate CDC28P on tyrosine and inhibit its activity |
| 420 | YDR387C | - | 2.3225348 | 2.4746572 | 3.0481024 | Protein with similarity to ITR1P and ITR2P |
| 421 | YDR251W | (PAM1) | 2.09471237 | 2.4744652 | 2.3344613 | Coiled-coil protein and multicopy suppressor of loss of PP2A (genes PPH21, PPH22, and PPH3) |
| 422 | YJL172W | (CPS1) | 2.4464951 | 2.473092 | 2.228723 | GLY-X carboxypeptidase YSCS, involved in nitrogen metabolism |
| 423 | YMR277W | (FCP1) | 2.51675116 | 2.466666 | 2.2346158 | TFIIF-interacting component of the C-terminal domain phosphatase |
| 424 | YDL047W | (SIT4) | 2.40214863 | 2.4572974 | 2.7529791 | Protein serine/threonine phosphatase involved in cell cycle regulation, member of the PPP family of protein phosphatases and related to PP2A phosphatases |
| 425 | YML117W | - | 2.2473701 | 2.4482108 | 2.8054783 | Protein of unknown function, contains an ATP/GTP-binding site motif A (P-loop) |
| 426 | YHR039C-A | - | 2.49103418 | 2.4469729 | 1.7368373 | - |
| 427 | YLL003W | (SFI1) | 3.03031186 | 2.4467012 | 2.2685901 | Protein of unknown function |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 428 | YKR048C | (NAP1) | 3.02222721 | 2.4404483 | 3.002619 | Nucleosome assembly protein that plays a role in assembly of histones into octamer, required for full expression of CLB2P functions |
| 429 | YOR197W | - | 2.87645711 | 2.438206 | 1.9784081 | Protein of unknown function |
| 430 | YEL046C | (GLY1) | 2.40664526 | 2.4369367 | 2.6795853 | Protein required for glycine prototrophy in SHMT1 SHMT2 double mutant |
| 431 | YJL029C | - | 2.36823878 | 2.43429 | 2.3384644 | Protein of unknown function, has similarity to C. elegans hypothetical protein T05G5.8 |
| 432 | YOR233W | (KIN4) | 3.52231883 | 2.4312627 | 3.0678435 | Serine/threonine protein kinase related to KIN1P and KIN2P, catalytic domain is most related to SNF1P |
| 433 | YOR299W | (BUD7) | 2.16058794 | 2.4312223 | 2.9585581 | Protein required for bipolar budding pattern |
| 434 | YHR218W | - | 2.37694362 | 2.4297245 | 4.1990669 | Protein with similarity to other subtelomerically-encoded proteins including YHR219P and YFL065P, probable pseudogene |
| 435 | YGL026C | (TRP5) | 3.92053304 | 2.4267316 | 2.4752996 | Tryptophan synthase, last (fifth) step in tryptophan biosynthesis pathway |
| 436 | YJL017W | - | 2.745014 | 2.4179146 | 2.8613495 | Protein of unknown function |
| 437 | YNL161W | - | 4.7525671 | 2.4161417 | 2.324762 | Serine/threonine protein kinase of unknown function |
| 438 | YOR141C | (ARP8) | 5.68817037 | 2.4122798 | 1.7395537 | Protein with similarity to actin and actin-related proteins ARP1P-ARP10P |
| 439 | YAL042W | - | 2.84377325 | 2.4057529 | 3.7961408 | Protein of unknown function, has 2 potential transmembrane domains |
| 440 | YGR270W | (YTA7) | 2.68803581 | 2.4056715 | 1.945755 | Protein with similarity to members of the AAA family of ATPases |
| 441 | YBR119W | (MUD1) | 2.83912216 | 2.4051525 | 1.3987642 | U1 SNRNP A protein (SNRNA-associated protein) with 2 RNA recognition (RRM) domains |
| 442 | YDR052C | (DBF4) | 6.85835185 | 2.4036928 | 1.5834976 | Regulatory subunit for CDC7P protein kinase, required for G1/S transition |
| 443 | YEL069C | (HXT13) | 2.69020108 | 2.4013304 | 3.6711431 | Protein with strong similarity to hexose transporters, member of the sugar permease family |
| 444 | YDR285W | (ZIP1) | 8.03633767 | 2.3921886 | 0.2216256 | Structural protein of the synaptonemal element central element, has predicted coiled-coil domain |
| 445 | YJL047C | - | 2.8960182 | 2.3885065 | 2.0814157 | Protein with similarity to clathrin heavy chain in one domain |
| 446 | YKL101W | (HSL1) | 4.2235071 | 2.3780286 | 2.4485279 | Serine/threonine protein kinase that interacts genetically with histone mutations |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 447 | YIL143C | (SSL2) | 2.16202858 | 2.3668818 | 1.9944618 | DNA helicase component of RNA polymerase transcription initiation factor TFIIH (factor B) |
| 448 | YBR182C | - | 3.15043584 | 2.3653183 | 2.517131 | - |
| 449 | YER189W | - | 2.65287612 | 2.3630614 | 5.1724275 | Protein with similarity to subtelomerically-encoded proteins including YIL177P, YHL049P, and YJL225P |
| 450 | YLR194C | - | 3.11287981 | 2.3617044 | 2.923307 | Protein of unknown function |
| 451 | YGR160W | - | 2.13853989 | 2.3577684 | 1.8132562 | Protein of unknown function |
| 452 | YGR258C | (RAD2) | 2.06944636 | 2.3572245 | 2.1751698 | Structure-specific single-stranded DNA endonuclease of the nucleotide excision repairosome |
| 453 | YGR162W | (TIF4631) | 2.28099935 | 2.3554791 | 1.7039222 | MRNA CAP-binding protein (EIF4F) 150K subunit |
| 454 | YJR036C | - | 3.21027204 | 2.3546452 | 5.0712893 | Possible ubiquitin-protein ligase (E3) |
| 455 | YGR124W | (ASN2) | 3.37829988 | 2.3505148 | 2.4742017 | Asparagine synthetase (L-aspartate: L-glutamine amidoligase [AMP-forming]), ASN1P and ASN2P are isozymes |
| 456 | YDL180W | - | 2.20643197 | 2.3467843 | 1.8047293 | Protein of unknown function |
| 457 | YDR266C | - | 3.29383065 | 2.3411759 | 2.3118864 | Protein of unknown function |
| 458 | YAR073W | - | 7.67257484 | 2.3325262 | 1.6890618 | Protein with strong similarity to PUR5P, may be an inosine-5'-monophosphate dehydrogenase |
| 459 | YPL048W | (CAM1) | 2.18528771 | 2.3294863 | 3.3106924 | - |
| 460 | YEL030W | (ECM10) | 1.99868799 | 2.3236082 | 2.3835153 | Protein possibly involved in cell wall structure or biosynthesis |
| 461 | YLL058W | - | 6.13836096 | 2.3223158 | 2.3541199 | Protein with similarity to neurospora crassa O-succinylhomoserine (thiol)-lyase |
| 462 | YJR010W | (MET3) | 8.36384636 | 2.3172147 | 1.5113084 | ATP-sulfurylase (sulfate adenylyltransferase) |
| 463 | YER110C | (KAP123) | 3.02732098 | 2.3160572 | 1.8042941 | Karyopherin-beta, involved in nuclear import of ribosomal proteins |
| 464 | YGL063W | (PUS2) | 2.17517427 | 2.3124794 | 4.1754638 | Pseudouridine synthase |
| 465 | YPL184C | - | 3.3404012 | 2.3122475 | 2.2563666 | Protein of unknown function |
| 466 | YGR254W | (ENO1) | 2.05650599 | 2.3095639 | 1.9054756 | Enolase 1 (2-phosphoglycerate dehydratase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis |
| 467 | YIL108W | - | 3.15926869 | 2.3086561 | 2.5782072 | Protein of unknown function |
| 468 | YDR388W | (RVS167) | 2.34115713 | 2.3058518 | 2.6912527 | Protein with A SH3 domain that affects actin distribution and bipolar budding |
| 469 | YNL323W | - | 2.29668952 | 2.3038327 | 2.0645985 | Protein with similarity to YCX1P |
| 470 | YBL076C | (ILS1) | 2.31635893 | 2.3036041 | 1.7634202 | Isoleucyl-TRNA synthetase |
| 471 | YLR217W | - | 2.57939547 | 2.2859565 | 1.6611523 | Protein of unknown function |
| 472 | YGR294W | - | 8.48668724 | 2.2857763 | 1.7132102 | Protein of the PAU1 family |
| 473 | YDL070W | - | 2.16064033 | 2.2854538 | 3.7599153 | - |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 474 | YOL044W | - | 2.15373467 | 2.2849315 | 2.1736446 | - |
| 475 | YGL145W | (TIP20) | 4.18903489 | 2.2829973 | 1.6161221 | Cytoplasmic protein that interacts physically with SEC20P, required for ER to Golgi transport |
| 476 | YLR044C | (PDC1) | 2.21772333 | 2.2774972 | 1.9431592 | Pyruvate decarboxylase isozyme 1 |
| 477 | YNR013C | - | 2.0080141 | 2.2770842 | 2.4893728 | Protein with similarity to PHO87P and YJL198P, member of the phosphate permease family of the major facilitator superfamily (MFS) |
| 478 | YML049C | - | 2.08547393 | 2.2761395 | 2.0329879 | - |
| 479 | YDR221W | - | 2.53153283 | 2.2731861 | 1.8131644 | Protein with similarity to the beta subunit of human glucosidase II |
| 480 | YMR135C | - | 4.75727106 | 2.2636411 | 4.3609747 | Protein of unknown function |
| 481 | YKR001C | (VPS1) | 2.48277065 | 2.2630712 | 1.5678763 | Vacuolar sorting protein, member of the dynamin family of GTPases |
| 482 | YLR413W | - | 2.80009402 | 2.2629262 | 2.3695083 | Protein of unknown function |
| 483 | YDR122W | (KIN1) | 2.0434064 | 2.2623436 | 2.3432635 | Serine/threonine protein kinase, related to KIN2P and S. pombe KIN1 |
| 484 | YIL154C | (IMP2') | 2.216207 | 2.2548739 | 2.2466776 | - |
| 485 | YKL068W | (NUP100) | 2.2598003 | 2.2529093 | 2.7012733 | Nuclear pore protein (nucleoporin) of the GLFG family, may be involved in binding and translation of proteins during nucleocytoplasmic transport |
| 486 | YHR190W | (ERG9) | 2.81318531 | 2.2475123 | 1.7238705 | Squalene synthetase (farnesyl-diphosphate farnesyltransferase), acts at a branch point in the isoprenoid biosynthesis pathway |
| 487 | YGL179C | - | 4.83814707 | 2.2398396 | 3.8786749 | Serine/threonine protein kinase with similarity to ELM1P and KIN82P |
| 488 | YOL017W | - | 3.01741322 | 2.2303862 | 2.2459064 | Protein of unknown function |
| 489 | YHR189W | - | 2.0021212 | 2.22911 | 2.2289936 | Putative peptidyl-TRNA hydrolase (PTH) |
| 490 | YNL208W | - | 3.64860898 | 2.2181817 | 2.5247363 | Protein of unknown function |
| 491 | YHR041C | (SRB2) | 2.27216109 | 2.2178582 | 2.4847273 | Component of the RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex |
| 492 | YPR080W | (TEF1) | 2.50402057 | 2.2115095 | 1.8587879 | Translation elongation factor EF-1alpha (TEF1 and TEF2 code for identical proteins) |
| 493 | YBR229C | (ROT2) | 2.45186053 | 2.2034499 | 2.1844611 | Catalytic (alpha) subunit of glucosidase II |
| 494 | YGR262C | - | 2.83275613 | 2.2029336 | 1.9251756 | Protein with similarity to apple tree calcium/calmodulin-binding protein kinase PIR:JQ2251 |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 495 | YER144C | (UBP5) | 3.38126089 | 2.1994294 | 2.7106303 | Ubiquitin-specific protease (ubiquitin C-terminal hydrolase), homologous to DOA4P and human TRE-2 |
| 496 | YDR264C | (AKR1) | 3.13151279 | 2.1983967 | 2.7516536 | Ankyrin repeat-containing protein that has an inhibitory effect on signaling in the pheromone pathway |
| 497 | YLR427W | - | 2.24985411 | 2.1938243 | 2.5059695 | Protein of unknown function |
| 498 | YLR374C | - | 2.26923061 | 2.1927227 | 2.6395044 | Protein of unknown function |
| 499 | YMR092C | (AIP1) | 2.2241966 | 2.1917074 | 2.1939749 | Actin interacting protein, has 4 WD (WD-40) repeats |
| 500 | YDR294C | - | 2.20085342 | 2.1899557 | 2.3333139 | - |
| 501 | YMR296C | (LCB1) | 2.1334221 | 2.1891645 | 1.9030014 | Component of serine C-palmitoyltransferase, first step in biosynthesis of long-chain base component of sphingolipids |
| 502 | YKR039W | (GAP1) | 1.99105648 | 2.1881751 | 1.2556866 | General amino acid permease, proton symport transporter for all naturally-occurring L-amino acids, 4-aminobutyric acid (GABA), ornithine, citrulline, some D-amino acids, and some toxic analogs |
| 503 | YDR422C | (SIP1) | 2.62373247 | 2.1870761 | 2.0836347 | Multicopy suppressor of SNF1, related to GAL83P/SPM1P and SPM2P |
| 504 | YMR080C | (NAM7) | 2.82340116 | 2.1828046 | 2.1714828 | Protein involved with NMD2P and UPF3P in decay of MRNA containing nonsense codons |
| 505 | YBL106C | - | 2.38138747 | 2.1809814 | 2.7798326 | - |
| 506 | YEL043W | - | 3.44125375 | 2.1784956 | 2.8076042 | Protein of unknown function |
| 507 | YBR222C | (FAT2) | 5.13679804 | 2.1781103 | 3.0936394 | Peroxisomal AMP-binding protein |
| 508 | YDR004W | (RAD57) | 2.26389978 | 2.1754266 | 2.076582 | Component of recombinosome complex involved in meiotic recombination and recombinational repair, with RAD55P promotes DNA strand exchange by RAD51P recombinase |
| 509 | YHR174W | (ENO2) | 2.38714668 | 2.1702816 | 1.9697417 | Enolase 2 (2-phosphoglycerate dehydratase), converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis |
| 510 | YER043C | (SAH1) | 3.73200717 | 2.1669937 | 1.6246235 | Adenosylhomocysteinase (S-adenosylhomocysteine hydrolase) |
| 511 | YKR012C | - | 2.41358469 | 2.1555775 | 1.1414615 | Protein of unknown function |
| 512 | YOL007C | - | 3.17872347 | 2.1529948 | 1.2712945 | - |
| 513 | YMR220W | (ERG8) | 2.68816133 | 2.1489328 | 2.0693924 | Phosphomevalonate kinase, converts mevalonate-5-phosphate to mevalonate pyrophosphate, involved in isoprene and ergosterol biosynthesis pathways |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 514 | YDR062W | (LCB2) | 2.54448949 | 2.1430094 | 1.9627647 | Subunit of serine C-palmitoyltransferase, first step in sphingolipic biosynthesis, and suppressor of calcium-sensitivity of CSG2 |
| 515 | YAL048C | - | 5.02313141 | 2.1384748 | 4.221132 | Protein with weak similarity to RAS1P, RAS2P, and other GTP-binding proteins of the RAS superfamily |
| 516 | YBL111C | - | 2.17340644 | 2.1313903 | 3.8030907 | - |
| 517 | YJL108C | - | 4.56646166 | 2.1302533 | 2.8609713 | Protein of unknown function, contains 8 potential transmembrane domains |
| 518 | YJL141C | (YAK1) | 2.80000608 | 2.1277388 | 2.8291776 | Serine/threonine protein kinase, negative regulator of cell growth acting in opposition to CAMP-dependent protein kinase A |
| 519 | YJL102W | (MEF2) | 2.08592026 | 2.1220696 | 1.6098307 | Mitochondrial translation elongation factor, promotes GTP-dependent translocation of nascent chain from A-site to P-site of ribosome |
| 520 | YDL174C | (DLD1) | 2.28050309 | 2.1220649 | 2.4305801 | D-lactate dehydrogenase (cytochrome), (D-lactate ferricytochrome C oxidoreductase) (D-LCR), mitochondrial |
| 521 | YMR011W | (HXT2) | 7.25080973 | 2.1188378 | 1.6420019 | High-affinity hexose transporter, member of sugar permease family |
| 522 | YLR129W | (DIP2) | 3.36115373 | 2.1126408 | 2.0325416 | DOM34P-interacting protein, has WD (WD-40) repeats |
| 523 | YML008C | (ERG6) | 2.51872662 | 2.1091692 | 1.7889829 | S-adenosylmethionine delta-24-sterol-C-methyltransferase, carries out methylation of zymosterol as part of the ergosterol biosynthesis pathway |
| 524 | YGL245W | - | 2.30162026 | 2.1065078 | 1.4267053 | Glutamyl-TRNA synthetase, member of the Class I aminoacyl TRNA synthetase family |
| 525 | YGL024W | - | 2.67631735 | 2.1046757 | 1.4610387 | Protein of unknown function |
| 526 | YHL027W | (RIM101) | 2.57210755 | 2.1033157 | 2.5927892 | Zinc-finger protein involved in induction of IME1 |
| 527 | YGR281W | (YOR1) | 4.18259907 | 2.0935061 | 2.3634092 | Oligomycin-resistance factor, member of the ATP-binding cassette (ABC) superfamily |
| 528 | YIL175W | - | 2.10803474 | 2.0859355 | 2.4771166 | - |
| 529 | YHL019C | (APM2) | 1.9986708 | 2.0848729 | 3.0618718 | Clathrin-associated protein (AP) complex, medium subunit |
| 530 | YAL019W | (FUN30) | 5.19927199 | 2.0806959 | 1.7340212 | - |
| 531 | YGL112C | (TAF60) | 2.21463331 | 2.0765265 | 2.1891308 | Component of TAF(II) complex (TBP-associated protein complex) required for activated transcription by RNA polymerase II |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 532 | YNL218W | - | 2.28887465 | 2.0761 | 1.6749939 | Protein with similarity to E. coli DNA polymerase III gamma and TAU subunits |
| 533 | YML058C-A | - | | 217.969407 | 2.0723568 | 3.2869214 |
| 534 | YOL156W | (HXT11) | 5.12784966 | 2.0709411 | 2.2192118 | Low-affinity glucose permease |
| 535 | YGR218W | (CRM1) | 2.32581989 | 2.0675233 | 1.5505702 | Exportin, beta-karyopherin |
| 536 | YGR296W | - | 3.15948331 | 2.0664535 | 3.7402619 | Protein with similarity to other subtelomerically-encoded proteins including YER190P (YPL283 and YGR296W code for identical proteins) |
| 537 | YLR176C | - | 2.54329087 | 2.0627475 | 1.4892288 | - |
| 538 | YDL229W | (SSB1) | 5.21935107 | 2.0615889 | 2.0067653 | Heat shock protein of HSP70 family involved in the translational apparatus |
| 539 | YER034W | - | 2.57654853 | 2.0562947 | 1.9025056 | Protein of unknown function |
| 540 | YKR050W | (TRK2) | 2.23638067 | 2.056259 | 4.703529 | Potassium transporter of the plasma membrane, moderate affinity, member of the potassium permease family of the major facilitator superfamily |
| 541 | YIL113W | - | 7.07756282 | 2.0539759 | 2.28618 | Dual-specificity protein phosphatase |
| 542 | YCR023C | - | 2.01851078 | 2.0520751 | 2.2109695 | Member of major facilitator superfamily (MFS) multidrug-resistance protein family 2 |
| 543 | YMR069W | - | 4.45745957 | 2.0520592 | 0 | Protein of unknown function |
| 544 | YAL020C | (ATS1) | 3.02597511 | 2.050802 | 2.0781706 | Protein with similarity to human RCC1 protein, suppressor of mutations in alpha tubulin |
| 545 | YNL256W | - | 3.16308725 | 2.045577 | 1.8697374 | Protein with similarity to bacterial dihydropteroate synthase |
| 546 | YMR124W | - | 2.65610298 | 2.0431312 | 2.2988806 | Protein of unknown function, has potential coiled-coil region (GB:Z49273) |
| 547 | YOR162C | - | 2.4478098 | 2.0361958 | 2.1075035 | - |
| 548 | YOR353C | - | 2.20965265 | 2.0220258 | 1.7471747 | Protein with weak similarity to adenylate cyclases |
| 549 | YPL028W | (ERG10) | 2.86559138 | 2.0185951 | 1.6989337 | Acetyl-COA acetyltransferase (acetoacetyl-COA thiolase), first step in mevalonate/sterol pathway |
| 550 | YIL114C | (POR2) | 2.24322702 | 2.0152799 | 2.367678 | Outer mitochondrial membrane porin (voltage-dependent anion-selective channel) |
| 551 | YDL029W | (ACT2) | 2.07186888 | 2.0140172 | 1.810394 | - |
| 552 | YDL143W | (CCT4) | 2.3041307 | 2.0128325 | 1.6478427 | Component of chaperonin-containing T-complex (TCP ring complex, TRIC), homologous to mouse CCT4 |
| 553 | YPL267W | - | 2.06501413 | 2.0119076 | 1.6761922 | Protein of unknown function |
| 554 | YOL105C | - | 2.79225712 | 2.0026061 | 2.23737 | - |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 555 | YML004C | (GLO1) | 2.19630894 | 2.0015677 | 1.7985136 | Glyoxalase I, converts methylglyoxal and glutathione into S-D-lactoylglutathione |
| 556 | YMR266W | - | 2.47393267 | 1.991188 | 1.727182 | Protein of unknown function, probable integral membrane glycoprotein |
| 557 | YPL194W | - | 2.87006368 | 0.4961465 | 1.5346869 | - |
| 558 | YOR152C | - | 2.74047761 | 0.4915256 | 0.2221023 | Protein of unknown function |
| 559 | YDR242W | (AMD2) | 8.28951711 | 0.4819032 | 0.9215489 | Protein with similarity to amidases |
| 560 | YFL054C | - | 7.43223753 | 0.4793582 | 0.6136582 | Protein with similarity to FPS1P and YPR192P, member of MIP family of transmembrane channels |
| 561 | YAR068W | - | 3.24259317 | 0.479021 | 1.2297001 | Protein with similarity to ICWP protein |
| 562 | YAL001C | (TFC3) | 2.94740587 | 0.4742746 | 1.1915566 | RNA polymerase transcription initiation factor TFIIIC (TAU), 138 KDA subunit |
| 563 | YLR454W | - | 5.72921213 | 0.4716283 | 1.641906 | Protein of unknown function |
| 564 | YDL020C | (SON1) | 2.27378766 | 0.4591519 | 0.8208918 | - |
| 565 | YMR225C | (MRPL44) | 0.19372389 | 0.4430311 | 0.4019617 | Mitochondrial ribosomal protein of the large subunit (YMR44) |
| 566 | YJR038C | - | 9.06373624 | 0.4422872 | 4.1801655 | Protein of unknown function |
| 567 | YDR380W | - | 0.1136124 | 0.4417559 | 0.8241167 | Protein with similarity to pyruvate decarboxylase, pyruvate oxidase, acetolactate synthase (large subunit), and other enzymes that require thiamine pyrophosphate |
| 568 | YKL170W | (MRPL38) | 0.20347891 | 0.4296401 | 0.4533368 | Mitochondrial ribosomal protein of the large subunit (YML38) (E. coli L14), belongs to the L14 family of prokaryotic ribosomal proteins |
| 569 | YGR248W | (SOL4) | 0.17664863 | 0.4293198 | 0.4062793 | Protein of unknown function |
| 570 | YER058W | (PET117) | 0.18996331 | 0.4289442 | 0.4202828 | Protein involved in assembly of cytochrome oxidase |
| 571 | YBR039W | (ATP3) | 0.18787084 | 0.4197886 | 0.2837245 | F1-gamma ATP synthase |
| 572 | YDL102W | (CDC2) | 17.5853214 | 0.4169873 | 0.0258767 | - |
| 573 | YJR153W | - | 3.65551445 | 0.4116558 | 0.6086987 | - |
| 574 | YMR188C | - | 0.20743995 | 0.4113817 | 0.3381207 | Protein with similarity to 30S ribosomal proteins (S17) |
| 575 | YBR244W | - | 0.16093632 | 0.4035137 | 0.3438917 | Protein with similarity to glutathione peroxidase |
| 576 | YDR523C | (SPS1) | 10.8815611 | 0.4014712 | 0.3371725 | Serine/threonine protein kinase involved in middle/late stage of meiosis |
| 577 | YDL031W | - | 2.0561223 | 0.3989968 | 0.6791327 | Protein with similarity to RNA helicases of dead/DEAH box family |
| 578 | YER109C | (FLO8B) | 2.33584341 | 0.3826502 | 2.0529509 | - |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 579 | YIR017C | (MET28) | 2.97658904 | 0.3775372 | 0.3008895 | Transcriptional activator of the basic leucine zipper (BZIP) family, works with MET4P and CBF1P to regulation sulfur amino acid metabolism |
| 580 | YDL016C | - | 3.9417341 | 0.374232 | 0.2672688 | Protein of unknown function |
| 581 | YIR028W | (DAL4) | 2.5006493 | 0.3741716 | 3.0010653 | Allantoin permease, member of the uracil/allantoin permease family of the major facilitator superfamily (MFS) |
| 582 | YOR124C | (UBP2) | 2.8382974 | 0.3622925 | 0.3859773 | Ubiquitin-specific protease (ubiquitin C-terminal hydrolase), cleaves at the C-terminus of ubiquitin |
| 583 | YBL108W | - | 0.1900473 | 0.3575329 | 0.5467376 | Protein of unknown function |
| 584 | YDR259C | - | 5.62713626 | 0.3429355 | 0.2335082 | - |
| 585 | YDR253C | (MET32) | 2.86314943 | 0.3397175 | 0.3279043 | Zinc-finger protein involved in transcriptional regulation of methionine metabolism |
| 586 | YJL196C | (ELO1) | 0.17135352 | 0.3378086 | 0.3752547 | Fatty acid elongation protein involved in elongation of tetradecanoic acid to hexadecanoic acid |
| 587 | YDR141C | - | 0.09160554 | 0.3290633 | 0.1693929 | Protein of unknown function, member of the major facilitator superfamily (MFS) |
| 588 | YBR069C | (VAP1) | 3.0181038 | 0.3157547 | 1.2268269 | Amino acid permease for valine, leucine, isoleucine, tyrosine, and tryptophan |
| 589 | YOR314W | - | 2.65430513 | 0.2917342 | 0.3312621 | Protein of unknown function |
| 590 | YDL068W | - | 0.11556176 | 0.2684108 | 0.1521109 | Protein of unknown function |
| 591 | YPL136W | - | 2.17418921 | 0.2530647 | 3.1708409 | Protein of unknown function |
| 592 | YGL034C | - | 0.1411795 | 0.2524039 | 0.3723439 | Protein of unknown function |
| 593 | YLR162W | - | 4.13626663 | 0.2515583 | 0.6851592 | Protein of unknown function |
| 594 | YMR193C-A | - | 3.34099753 | 0.2354896 | 0.3596816 | - |
| 595 | YMR146C | (TIF34) | 5.0351989 | 0.2248204 | 0.7193538 | Translation initiation factor EIF3, P39 subunit, has 2 WD (WD-40) repeats |
| 596 | YFL012W | - | 71.9436495 | 0.2235373 | 1.5215902 | Protein of unknown function |
| 597 | YER096W | - | 7.21258235 | 0.1766673 | 0.4170679 | - |
| 598 | YNR071C | - | 2.01488788 | 0.1446196 | 0.0535063 | Protein with similarity to UDPglucose 4-epimerase |
| 599 | YLR419W | - | 0.20769335 | 0.1102431 | 0.9141258 | Protein with similarity to several pre-MRNA splicing factors |
| 600 | YKL105C | - | 3.23146223 | 0.086572 | 5.0836556 | Protein of unknown function |
| 601 | YLR142W | (PUT1) | 2.2907881 | 0.0854218 | 0.6671487 | Proline oxidase, first step in synthesis of glutamate from proline |
| 602 | YDL239C | - | 7.81000565 | 0.0417738 | 0.347901 | Protein of unknown function |
| 603 | YHR137W | (ARO9) | 0.07724918 | 0.0347684 | 0.0703134 | Aromatic amino acid aminotransferase II |
| 604 | YDR374C | - | 17.25276 | 0 | 4.6059679 | Protein of unknown function |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 605 | YIL100W | - | 9.97598883 | 0 | 2.8122773 | Protein of unknown function, questionable ORF |
| 606 | YPL025C | - | 9.52247441 | 0 | 20.22382 | Protein of unknown function |
| 607 | YOR072W | - | 7.48662389 | 0 | 6.2287404 | Protein of unknown function |
| 608 | YNL242W | - | 6.47720448 | 0 | 2.5753253 | Protein of unknown function |
| 609 | YIR027C | (DAL1) | 5.64113227 | 0 | 0 | Allantoinase, first step in the degradation of allantoin as a secondary nitrogen source |
| 610 | YOR139C | - | 5.46648132 | 0 | 11.760995 | Transcription factor with domains homologous to MYC oncoprotein and yeast HSF1P, required for normal cell surface assembly and flocculence |
| 611 | YEL019C | (MMS21) | 3.34008483 | 0 | 2.069236 | Protein involved in DNA repair |
| 612 | YDL132W | (cdc53) | 3.16426832 | 0 | 0.1467847 | - |
| 613 | YOR177C | - | 2.97842594 | 0 | 0.435871 | Protein of unknown function |
| 614 | YML042W | (CAT2) | 2.76437696 | 0 | 16.65885 | Carnitine O-acetyltransferase, peroxisomal and mitochondrial |
| 615 | YER044C-A | (MEI4) | 2.5971776 | 0 | 0 | Protein required early in meiosis for meiotic recombination, chromosome synapsis, and viable spore formation |
| 616 | YGR083C | (GCD2) | 2.32134339 | 0 | 0 | Translation initiation factor EIF2B (guanine nucleotide exchange factor), 71 KDA (delta) subunit |
| 617 | YAR030C | - | 2.06301879 | 0 | 0 | Protein of unknown function, probable non-coding ORF |
| 618 | YJR157W | - | 0.2073771 | 0 | 0.6711879 | Protein of unknown function |
| 619 | YHR217C | - | 0.2061042 | 0 | 0.549346 | Protein of unknown function |
| 620 | YKL100C | - | 0.12715731 | 0 | 40.399169 | Protein of unknown function |

\* Table Headings:

Clone ID: A clone ID designation number.

Alias: Alternative gene names used in the literature. This information is provided

5    by YPD™, Hodges *et al. Nucl. Acids Res. 27:* 69-73 (1999), the entirety of

which is herein incorporated by reference.

CJ-4hr/LP-4hr: Expression level in the mutant CJ517 as compared with the

respective wild type strain LPY9 at 4hr sampling of log phase growth of yeast

(ratio of mutant expression level/control expression level). CJ refers to the

10   mutant CJ517 (The mutant is defective in the gene (ERG11) codes for C14

demethylase enzyme in the sterol biosynthetic pathway). LP refers to the

respective wild type strain LPY9, used to compare the gene expression profile with the mutant.

K-50/CK: Expression level in the wild type yeast LPY9, at 2 hr after treatment with 50micro gram/ml ketoconazole as compared to the wild type LPY9 strain without ketoconazole treatment (ratio of treatment expression level/control expression level). K refers to ketoconazole treatment. The clones listed in Table 2 are either up or down regulated in the mutant (CJ517) as well as in response to ketoconazole treatment.

K-100/CK: Expression level in the wild type yeast LPY9, at 2 hr after treatment with 100micro gram/ml ketoconazole as compared to the wild type LPY9 strain without ketoconazole treatment (ratio of treatment expression level/control expression level).

Gene Description: Description of the clone listed in column 1.

Table 3, below, lists the RNAs from Table 2 that correspond to genes or structural regions implicated in transcription regulation.

**Table 3***

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 30 | YOR237W | (HES1) | 134.648161 | 1417.62621 | 1358.12348 | Protein implicated in ergosterol biosynthesis, member of the KES1/HES1/OSH1/YKR003W family of oxysterol-binding (OSBP) proteins |
| 42 | YDR213W | - | 18.2079478 | 32.1360646 | 58.3586116 | Protein with similarity to transcription factors, has ZN[2]-CYS[6] fungal-type binuclear cluster domain in the N-terminal region |
| 74 | YGR177C | (ATF2) | 3.7081426 | 11.830167 | 12.5552685 | Alcohol O-acetyltransferase |
| 75 | YFR034C | (PHO4) | 14.8112083 | 11.2160731 | 20.8445145 | Basic helix-loop-helix (BHLH) transcription factor required for expression of phosphate pathway, hyperphosphorylation by PHO80P-PHO85P cyclin-dependent protein kinase complex causes inactivation |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 83 | YOL067C | (RTG1) | 30.4142081 | 10.0270648 | 27.3663295 | Basic helix-loop-helix (BHLH) transcription factor involved in inter-organelle communication between mitochondria, peroxisomes, and nucleus |
| 100 | YJL127C | (SPT10) | 4.01528284 | 7.83944269 | 10.0960266 | Protein that amplifies the magnitude of transcriptional regulation at various loci |
| 111 | YMR037C | (MSN2) | 6.80686734 | 6.42359685 | 7.66129891 | Zinc-finger transcriptional activator for genes involved in the multistress response and genes regulated through SNF1P |
| 118 | YCR048W | (ARE1) | 9.11370518 | 6.1039374 | 10.5312906 | Acyl-COA:sterol acyltransferase (sterol-ester synthetase) |
| 131 | YAL013W | (DEP1) | 8.79366086 | 5.54633863 | 6.42500999 | Regulator of phospholipid metabolism |
| 132 | YIL084C | (SDS3) | 1.99582364 | 5.54306878 | 6.90742248 | Suppressor of silencing defect |
| 157 | YKR034W | (DAL80) | 3.91750209 | 5.0436172 | 7.28385659 | GATA-type zinc finger transcriptional repressor for allantoin and 4-aminobutyric acid (GABA) catabolic genes |
| 172 | YLR098C | (CHA4) | 2.05280928 | 4.75643469 | 5.58664651 | Zinc-finger protein required for activation of CHA1, has A ZN[2]-CYS[6] fungal-type binuclear cluster domain |
| 180 | YDR389W | (SAC7) | 3.89197011 | 4.56095992 | 4.31431086 | GTPase-activating protein for RHO1P |
| 202 | YDL088C | (ASM4) | 4.39685251 | 4.17572645 | 3.32103404 | Suppressor of temperature-sensitive mutations in POL3P (DNA polymerase delta) |
| 206 | YBL005W | (PDR3) | 3.75060207 | 4.14490535 | 6.08273054 | Transcription factor related to PDR1P, contains A ZN[2]-CYS[6] fungal-type binuclear cluster domain in the N-terminal region |
| 242 | YGL071W | (RCS1) | 3.39203358 | 3.69630773 | 4.53101664 | Regulatory protein involved in iron uptake |
| 255 | YAR044W | (OSH1) | 4.12112011 | 3.624939 | 3.88396219 | Protein implicated in ergosterol biosynthesis, member of the KES1/HES1/OSH1/YKR003W family of oxysterol-binding (OSBP) proteins |
| 256 | YLR120C | (YAP3) | 6.14265883 | 3.62298451 | 4.42985615 | Transcription factor of the basic leucine zipper (BZIP) family, one of eight members of a novel fungal-specific family of BZIP proteins |
| 260 | YJR017C | (ESS1) | 2.98118086 | 3.55874146 | 3.22082555 | Processing/termination factor, involved in transcription termination or 3'-end processing of pre-MRNA |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 271 | YMR019W | (STB4) | 3.2576922 | 3.44146214 | 3.39764598 | SIN3P-binding protein, has ZN[2]-CYS[6] fungal-type binuclear cluster domain in the N-terminal region |
| 278 | YLR153C | (ACS2) | 3.45528019 | 3.37854457 | 3.12858117 | Acetyl-COA synthetase (acetate-COA ligase) |
| 289 | YPL119C | (DBP1) | 5.87199247 | 3.24642228 | 2.19736599 | ATP-dependent RNA helicase of dead box family, suppressor of SPP81/DED1 |
| 290 | YGL014W | - | 3.11296478 | 3.22942947 | 3.6382821 | Protein with pumilio repeats that is involved with MPT5P in relocalization of SIR3P and SIR4P from telomeres to the nucleolus |
| 296 | YGL192W | (IME4) | 2.89030953 | 3.17038103 | 6.47841053 | Positive transcription factor for IME1 and IME2, mediates control of meiosis by carrying signals regarding mating type (A/alpha) and nutritional status |
| 297 | YMR047C | (NUP116) | 2.56622055 | 3.17022339 | 4.77420515 | Nuclear pore protein (nucleoporin) of the GLFG family, may be involved in binding and translocation of nuclear proteins |
| 301 | YLR249W | (YEF3) | 3.59397167 | 3.14453335 | 2.63195398 | Translation elongation factor EF-3A, member of ATP-binding cassette (ABC) superfamily |
| 322 | YOR337W | (TEA1) | 2.13152473 | 2.97907151 | 4.82285812 | TY1 enhancer activator of the GAL4P-type family of DNA-binding proteins |
| 331 | YCR084C | (TUP1) | 2.40138822 | 2.92198431 | 3.27182635 | General repressor of transcription (with SSN6P), member of WD (WD-40) repeat family |
| 336 | YPL226W | - | 2.45263084 | 2.88856775 | 2.55579443 | Protein with similarity to members of the ATP-binding cassette (ABC) superfamily |
| 345 | YJR019C | (TES1) | 4.07777555 | 2.83032346 | 2.07248965 | Acyl-COA thioesterase |
| 346 | YBL008W | (HIR1) | 7.24580603 | 2.82847131 | 2.88668127 | Histone transcription inhibitor, required for periodic repression of 3 of the 4 histone gene loci and for autogenous repression of HTA1-HTB1 locus by H2A and H2B |
| 349 | YGL001C | - | 3.91981575 | 2.82148161 | 1.98527852 | Protein with similarity to nocardia SP. cholesterol dehydrogenase |
| 359 | YCL037C | (SRO9) | 8.35007693 | 2.78557477 | 2.39358801 | Suppressor of YPT6 null and RHO3 mutations |
| 367 | YDR088C | (SLU7) | 2.07293165 | 2.73396273 | 2.68767436 | Pre-MRNA splicing factor affecting 3' splice site choice, required only for the second catalytic step of splicing |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 376 | YBR289W | (SNF5) | 2.00671327 | 2.68812945 | 3.03861899 | Component of SWI/SNF global transcription activator complex, acts to assist gene-specific activators through chromatin remodeling |
| 400 | YPL237W | (SUI3) | 2.5966981 | 2.5628077 | 2.54794558 | Translation initiation factor EIF2beta subunit |
| 406 | YOR127W | (RGA1) | 3.85804733 | 2.53166489 | 2.56973414 | RHO-type GTPase-activating protein (GAP) for CDC42P |
| 416 | YFR009W | (GCN20) | 2.63782118 | 2.48595438 | 2.16133777 | Component of a protein complex required for activation of GCN2P protein kinase in response to amino acid starvation, member of ATP-binding cassette (ABC) superfamily |
| 417 | YDR211W | (GCD6) | 2.22567451 | 2.48354852 | 1.82406386 | Translation initiation factor EIF2B (guanine nucleotide exchange factor), 81 KDA (beta) subunit |
| 440 | YGR270W | (YTA7) | 2.68803581 | 2.4056715 | 1.94575504 | Protein with similarity to members of the AAA family of ATPases |
| 441 | YBR119W | (MUD1) | 2.83912216 | 2.40515252 | 1.39876418 | U1 SNRNP A protein (SNRNA-associated protein) with 2 RNA recognition (RRM) domains |
| 442 | YDR052C | (DBF4) | 6.85835185 | 2.40369283 | 1.58349756 | Regulatory subunit for CDC7P protein kinase, required for G1/S transition |
| 492 | YPR080W | (TEF1) | 2.50402057 | 2.21150946 | 1.85878786 | Translation elongation factor EF-1alpha (TEF1 and TEF2 code for identical proteins) |
| 496 | YDR264C | (AKR1) | 3.13151279 | 2.19839665 | 2.75165355 | Ankyrin repeat-containing protein that has an inhibitory effect on signaling in the pheromone pathway |
| 503 | YDR422C | (SIP1) | 2.62373247 | 2.18707608 | 2.08363472 | Multicopy suppressor of SNF1, related to GAL83P/SPM1P and SPM2P |
| 504 | YMR080C | (NAM7) | 2.82340116 | 2.1828046 | 2.17148277 | Protein involved with NMD2P and UPF3P in decay of MRNA containing nonsense codons |
| 515 | YAL048C | - | 5.02313141 | 2.13847476 | 4.22113197 | Protein with weak similarity to RAS1P, RAS2P, and other GTP-binding proteins of the RAS superfamily |
| 526 | YHL027W | (RIM101) | 2.57210755 | 2.10331571 | 2.59278915 | Zinc-finger protein involved in induction of IME1 |
| 531 | YGL112C | (TAF60) | 2.21463331 | 2.07652653 | 2.18913076 | Component of TAF(II) complex (TBP-associated protein complex) required for activated transcription by RNA polymerase II |
| 549 | YPL028W | (ERG10) | 2.86559138 | 2.01859514 | 1.69893374 | Acetyl-COA acetyltransferase (acetoacetyl-COA thiolase), first step in mevalonate/sterol pathway |

| Seq. Num. | Clone ID | ALIAS | CJ-4hr/ LP-4hr | K-50/CK | K-100/CK | Gene Description |
|---|---|---|---|---|---|---|
| 621 | YNR019W | (ARE2) | 2.1 | 1.79103463 | 2.85442 | Acyl-COA:sterol acyltransferase (sterol-ester synthetase) |
| 560 | YFL054C | - | 7.43223753 | 0.47935821 | 0.61365816 | Protein with similarity to FPS1P and YPR192P, member of MIP family of transmembrane channels |
| 562 | YAL001C | (TFC3) | 2.94740587 | 0.47427458 | 1.19155655 | RNA polymerase transcription initiation factor TFIIIC (TAU), 138 KDA subunit |
| 579 | YIR017C | (MET28) | 2.97658904 | 0.3775372 | 0.30088953 | Transcriptional activator of the basic leucine zipper (BZIP) family, works with MET4P and CBF1P to regulation sulfur amino acid metabolism |
| 585 | YDR253C | (MET32) | 2.86314943 | 0.33971751 | 0.32790428 | Zinc-finger protein involved in transcriptional regulation of methionine metabolism |
| 595 | YMR146C | (TIF34) | 5.0351989 | 0.22482039 | 0.71935381 | Translation initiation factor EIF3, P39 subunit, has 2 WD (WD-40) repeats |
| 616 | YGR083C | (GCD2) | 2.32134339 | 0 | 0 | Translation initiation factor EIF2B (guanine nucleotide exchange factor), 71 KDA (delta) subunit |
| 610 | YOR139C | (SFL1) | 5.46648132 | 0 | 11.7609951 | Transcription factor with domains homologous to MYC oncoprotein and yeast HSF1P, required for normal cell surface assembly and flocculence |

* Table Headings:

Clone ID: A clone ID designation number.

CJ-4hr/LP-4hr: Expression level in the mutant CJ517 as compared with the respective wild type strain LPY9 at 4hr sampling of log phase growth of yeast (ratio of mutant expression level/control expression level). Genes in the Table are either up or down regulated in the mutant (CJ517) as well as in response to ketoconazole treatment.

K-50/CK: Expression level in the wild type yeast LPY9, at 2 hr after treatment with 50micro gram/ml ketoconazole as compared to the wild type LPY9 strain without ketoconazole treatment (ratio of treatment expression level/control expression level).

K-100/CK: Expression level in the wild type yeast LPY9, at 2 hr after treatment with 100micro gram/ml ketoconazole as compared to the wild type LPY9 strain without ketoconazole treatment (ratio of treatment expression level/control expression level).

5      Gene Description: Description of the clone listed in column 1.

In addition, for example, Table 2 identifies a yeast HES1 gene as a gene with an associated change in mRNA levels in the two different comparisons. Fang *et al. EMBO J* 15:6447-59 (1996), the entirety of which is herein incorporated by reference, reported a mutation in *HES1*, which caused a 55% reduction in carbon flux through the mevalonate pathway in yeast.

10     Each of the sequences listed in Table 2 or 3 represents a gene that effects sterol levels, directly or indirectly, or whose expression changes as a result of alterations in the sterol synthesis pathway.

**Example 2**

Sequences that encode for the yeast HES1 protein are used to search databases for

15     homologues from other species. A number of different databases can be used for these searches, including, for example, dbEST, GenBank, EMBL, SwissProt, PIR, and GENES. In addition, various algorithms for searching can be selected, such as, for example, the BLAST suite of programs at the default values. Typically, matches found with BLAST P values equal or less than 0.001 (probability) or BLAST Score of equal or greater than 90 are classified as hits. If the

20     program used to determine the hit is HMMSW then the score refers to HMMSW score. The GenBank database is searched with BLASTN and BLASTX (default values). Sequences that pass the hit probability threshold of $10e^{-8}$ are considered hits.

**Table 4**

| Seq. Num. | Clone ID | Sequence: DNA/Protein | Hit description | Library |
|---|---|---|---|---|
| 1 | 701100307CPR9855 | DNA | Yeast HES 1 homolog | SOYMON028 |
| 2 | 701001443CPR9857 | DNA | Yeast HES 1 homolog | SOYMON018 |
| 3 | 701010572CPR9854 | DNA | Yeast HES 1 homolog | SOYMON019 |
| 4 | 701176735CPR9736 | DNA | Yeast HES 1 homolog | SATMONN05 |

| Seq. Num. | Clone ID | Sequence: DNA/Protein | Hit description | Library |
|---|---|---|---|---|
| 5 | Z75145 | DNA | Protein implicated in ergosterol biosynthesis, member of the KES1/HES1/OSH1/YKR003W family of oxysterol-binding (OSBP) proteins | - |
| 622 | 701100307CPR9855 | Protein | Yeast HES 1 homolog | SOYMON028 |
| 623 | 701001443CPR9857 | Protein | Yeast HES 1 homolog | SOYMON018 |
| 624 | 701010572CPR9854 | Protein | Yeast HES 1 homolog | SOYMON019 |
| 625 | 701176735CPR9736 | Protein | Yeast HES 1 homolog | SATMONN05 |
| 626 | Z75145 | Protein | Protein implicated in ergosterol biosynthesis, member of the KES1/HES1/OSH1/YKR003W family of oxysterol-binding (OSBP) proteins | - |
| 6 | 701003888H1 | DNA | Yeast HES 1 homolog | SOYMON019 |
| 7 | 701001351H1 | DNA | Yeast HES 1 homolog | SOYMON018 |
| 8 | 700672545H1 | DNA | Yeast HES 1 homolog | SOYMON006 |
| 9 | 700664054H1 | DNA | Yeast HES 1 homolog | SOYMON005 |
| 10 | 700665644H1 | DNA | Yeast HES 1 homolog | SOYMON005 |
| 11 | 700764248H1 | DNA | Yeast HES 1 homolog | SOYMON020 |
| 12 | 700851444H1 | DNA | Yeast HES 1 homolog | SOYMON023 |
| 13 | 700971910H1 | DNA | Yeast HES 1 homolog | SOYMON005 |
| 14 | 700652932H1 | DNA | Yeast HES 1 homolog | SOYMON003 |
| 15 | 700982894H1 | DNA | Yeast HES 1 homolog | SOYMON009 |
| 16 | 701120140H1 | DNA | Yeast HES 1 homolog | SOYMON037 |
| 17 | 701064234H1 | DNA | Yeast HES 1 homolog | SOYMON034 |
| 18 | 700954013H1 | DNA | Yeast HES 1 homolog | SOYMON022 |
| 19 | 701129375H1 | DNA | Yeast HES 1 homolog | SOYMON037 |
| 20 | 701043941H1 | DNA | Yeast HES 1 homolog | SOYMON032 |
| 21 | LIB24-114-Q1-E1-H8 | DNA | Arabidopsis HES 1 homolog | LIB24 |
| 22 | LIB22-016-Q1-E1-F3 | DNA | Arabidopsis HES 1 homolog | LIB22 |
| 23 | LIB25-101-Q1-E1-F1 | DNA | Arabidopsis HES 1 homolog | LIB25 |
| 24 | AA042357 | DNA | Arabidopsis HES 1 homolog | - |
| 25 | AA720163 | DNA | Arabidopsis HES 1 homolog | - |
| 26 | Z29936 | DNA | Arabidopsis HES 1 homolog | - |
| 27 | T76850 | DNA | Arabidopsis HES 1 homolog | - |
| 28 | T76580 | DNA | Arabidopsis HES 1 homolog | - |
| 29 | AA586043 | DNA | Arabidopsis HES 1 homolog | - |

Homologues to yeast HES1 are also identified in the following libraries: SOYMON003, SOYMON005, SOYMON006, SOYMON009, SOYMON018, SOYMON019, SOYMON020, SOYMON022, SOYMON028, SOYMON023, SOYMON032, SOYMON034, SOYMON027, SATMONN05, LIB22, LIB 24, and LIB 25 These libraries are prepared as follows:

The SATMONN05 cDNA library is a normalized library generated from maize (B73 x Mo17, Illinois Foundation Seeds, Champaign Illinois, U.S.A.) root tissue at the V6 development stage. Seeds are planted at a depth of approximately 3 cm into 2-3 inch peat pots containing Metro 200 growing medium. After 2-3 weeks growth they are transplanted into 10 inch pots containing the same growing medium. Plants are watered daily before transplantation and three

times a week after transplantation.  Peters 15-16-17 fertilizer is applied three times per week after

transplanting at a strength of 150 ppm N.  Two to three times during the lifetime of the plant,

from transplanting to flowering, a total of 900 mg Fe is added to each pot.  Maize plants are

grown in a greenhouse in 15 hr day/9 hr night cycles.  The daytime temperature is approximately

5    80°F and the nighttime temperature is approximately 70°F.  Supplemental lighting is provided by

1000 W sodium vapor lamps.  Tissue is collected when the maize plant is at the 6-leaf

development stage.  The root system is cut from the mature maize plant and washed with water

to free it from the soil.  The tissue is immediately frozen in liquid nitrogen and the harvested

tissue is then stored at −80°C until RNA preparation.  The RNA is purified from the stored

10    tissue.  The library is normalized in two rounds using conditions adapted from Soares *et al.*,

*Proc. Natl. Acad. Sci. (U.S.A.)* *91*:9928 (1994), the entirety of which is herein incorporated by

reference and Bonaldo *et al.*, *Genome Res. 6*: 791 (1996), the entirety of which is herein

incorporated by reference except that a significantly longer (48 -hours/round) reannealing

hybridization was used.  SATMON003 is a root tissue library from the same donor.

15         The SOYMON003 cDNA library is generated from soybean cultivar Asgrow 3244

(Asgrow Seed Company, Des Moines, Iowa U.S.A.) hypocotyl axis tissue from seedlings 2 day

after-imbibition.  Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots

containing Metromix 350 medium.  Trays are placed in an environmental chamber and grown at

12hr daytime/12hr nighttime cycles.  The daytime temperature is approximately 29°C and the

20    nighttime temperature approximately 24°C.  Soil is checked and watered daily to maintain even

moisture conditions.  Tissue is collected 2 days after the start of imbibition.  The 2 days after

imbibition samples are separated into 3 collections after removal of any adhering seed coat.  At 2

days after imbibition under the above conditions, the seedlings have significant expansion of the

axis and are close to emerging from the soil.  A few seedlings have cracked the soil surface and

25    exhibited slight greening of the exposed cotyledons.  The seedlings are washed in water to

remove soil, hypocotyl axis harvested and immediately frozen in liquid nitrogen.  The harvested

tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the

5  manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The

10  Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON005 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) hypocotyl axis tissue from seeds 6 hour

15  post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Tissue is collected 6 hours after the start of imbibition. The 6 hours after

20  imbibition sample is collected over the course of approximately 2 hours starting at 6 hours post imbibition. At the 6 hours after imbibition stage, not all cotyledons have become fully hydrated and germination. Radicle protrusion has not occurred. The seedlings are washed in water to remove soil, then the hypocotyl axis is harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the

25  stored tissue and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the

manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON006 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) cotyledons from seeds 6 hour post-imbibition. Seeds are planted at a depth of approximately 2cm into 2-3 inch peat pots containing Metromix 350 medium. Trays are placed in an environmental chamber and grown at 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Tissue is collected 6 hours after imbibition. The 6 hours after imbibition sample is collected over the course of approximately 2 hours starting at 6 hours post-imbibition. At the 6 hours after imbibition, not all cotyledons have become fully hydrated and germination. Radicle protrusionhas not occurred. The seedlings are washed in water to remove soil, then the cotyledon is harvested and immediately frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning

strategies exist. A number of cDNA library construction kits are commercially available. The

Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life

Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the

5    manufacturer.

The SOYMON009 cDNA library is generated from soybean cutlivar C1944 (USDA

Soybean Germplasm Collection, Urbana, Illinois U.S.A.) pod and seed tissue harvested 15 days

post-flowering. Pods from field grown plants are harvested 15 days post-flowering. The pods

are picked from all over the plant, placed into 14ml polystyrene tubes and immediately immersed

10    in dry-ice. Approximately 3g of pod tissue is harvested. The harvested tissue is then stored at –

80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is

constructed. The RNA is purified from the stored tissue and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL,

Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the

15    manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as

recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York

U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning

strategies exist. A number of cDNA library construction kits are commercially available. The

20    Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life

Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the

manufacturer.

The SOYMON018 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow

Seed Company, Des Moines, Iowa U.S.A.) leaf tissue harvested from plants grown in a field in

25    Jerseyville 45 and 55 days after flowering. Leaves from field grown plants are harvested 45 and

55 days after flowering from the fourth node. Approximately 27g and 33g of leaves are collected

from the 45 and 55 days after flowering plants, placed into 14ml polystyrene tubes and

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immediately immersed in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. Total RNA is prepared from the combination of equal amounts of leaf tissue from both time points and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON019 cDNA library is generated from soybean cultivars Cristalina (USDA Soybean Germplasm Collection, Urbana, Illinois U.S.A.) and FT108 (Monsoy, Brazil) (tropical germ plasma) root tissue. Roots are harvested from plants grown in an environmental chamber under 12hr daytime/12hr nighttime cycles. The daytime temperature is approximately 29°C and the nighttime temperature approximately 24°C. Soil is checked and watered daily to maintain even moisture conditions. Approximately 50g and 56g of roots are harvested from each of the Cristalina and FT108 cultivars and immediately frozen in dry ice. The plants are uprooted and the roots quickly rinsed in a pail of water. The root tissue is then cut from the plants, placed immediately in 14ml polystyrene tubes and immersed in dry-ice. The harvested tissue is then stored at −80°C until RNA preparation. Total RNA is prepared from the combination of equal amounts of root tissue from each cultivar and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as

recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON020 cDNA is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) seeds harvested from plants grown in a field in Jerseyville 65 and 75 days post-flowering. The seed pods are picked from all over the plant and the seeds extracted from the pods. Approximately 14g and 31g of seeds are harvested from the respective seed pods and immediately frozen in dry ice. The harvested tissue is then stored at − 80°C until RNA preparation. Total RNA is prepared from the combination of equal numbers of seeds from 65 and 75 days after flowering and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON022 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) partially to fully opened flower tissue, which is harvested from plants grown in an environmental chamber. Seeds are planted in moist

Metromix 350 medium at a depth of approximately 2cm. Trays are placed in an environmental chamber set to a 12h day/12h night cycle, 29°C daytime temperature, 24°C night temperature and 70% relative humidity. Daytime light levels are measured at 450μEinsteins/m$^2$. Soil is checked and watered daily to maintain even moisture conditions. Flowers are removed from the plant at the pedicel. Flower buds showing petal color to fully open flowers are selected for collection. A total of 3g of flower tissue is harvested and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. Total RNA is prepared from a mixture of opened and partially opened flowers and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON023 cDNA library is generated from soybean genotype BW211S Null (Tohoku University, Morioka, Japan) seed tissue harvested from plants grown in a field in Jerseyville. After 15 and 40 days, pods are harvested from all over the plant and seeds are dissected out from the pods. Approximately, 0.7g and 14.2g of seeds are harvested from the plants at the 15 and 40 days after flowering timepoints. The seeds are placed into 14ml polystyrene tubes and immersed in dry-ice. The tissue is then transferred to a -80°C freezer for storage. The harvested tissue is then stored at −80°C until RNA preparation. Total RNA is prepared from the combination of 0.5g and 1.0g of seeds from the 15 and 40 days after flowering timepoints and the cDNA library is constructed.

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The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York

5    U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the

10    manufacturer.

The SOYMON028 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) drought-stressed root tissue. Seeds are planted in moist Metromix 350 medium at a depth of approximately 2cm in trays. The trays are placed in an environmental chamber set to a 12h day/12h night cycle, 26°C daytime temperature,

15    21°C night temperature and 70% relative humidity. Daytime light levels are measured at $300\mu$Einsteins/m$^2$. Soil is checked and watered daily to maintain even moisture conditions. At the R3 stage of development, water is withheld from half of the plant collection (drought stressed population). After 3 days, half of the plants from the drought stressed condition and half of the plants from the control population are harvested. After another 3 days (6 days post drought

20    induction) the remaining plants are harvested. A total of 27g and 40g of root tissue is harvested from plants at two time points and immediately frozen in dry ice. The harvested tissue is then stored at −80°C until RNA preparation. Total RNA is prepared from the combination of equal amounts of drought stressed root tissue from both time points and the cDNA library is constructed.

25    The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as

recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON032 cDNA library is prepared from the Asgrow cultivar A4922 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) rehydrated dry soybean seed meristem tissue. Surface sterilized seeds are germinated in liquid media for 24 hours. The seed axis is then excised from the barely germinating seed, placed on tissue culture media and incubated overnight at 20°C in the dark. The supportive tissue is removed from the explant prior to harvest. Approximately 570mg of tissue is harvested and frozen in liquid nitrogen. The harvested tissue is then stored at −80°C until RNA preparation. The RNA is purified from the stored tissue and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON034 cDNA library is generated from soybean cultivar Asgrow 3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) cold-shocked seedling tissue without

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cotyledons. Seeds are imbibed and germinated in vermiculite for 2 days under constant illumination (*ca.* 510 Lux). After 48 hours, the seedlings are transferred to a cold room set at 5°C under constant illumination (*ca.* 560 Lux). After 30, 60 and 180 minutes seedlings are harvested and dissected. The seedlings after 2 days of imbibition are beginning to emerge from the

5 vermiculite surface. The apical hooks are dark green in appearance. A portion of the seedling consisting of the root, hypocotyl and apical hook is frozen in liquid nitrogen and stored at −80°C. Total RNA is prepared from equal amounts of pooled tissue and the cDNA library is constructed.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the

10 manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The

15 Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The SOYMON037 cDNA library is generated from soybean cultivar A3244 (Asgrow Seed Company, Des Moines, Iowa U.S.A.) etiolated axis and radical tissue. Seeds are planted in

20 moist vermiculite, wrapped and kept at room temperature in complete darkness until harvest. Etiolated axis and hypocotyl tissue is harvested at 2, 3 and 4 days post-planting. Samples are frozen in liquid nitrogen upon harvesting and stored at -80°C until RNA preparation. 1 gram of each sample (axis + hypocotyl at day 2, 3 and 4) is pooled for RNA isolation. The RNA is purified from the pooled tissue and the cDNA library is constructed.

25 The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as

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recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The

5    Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The cDNA library of the present invention designated LIB22, is prepared from *Arabidopsis thaliana* Columbia ecotype root tissue. Wild type *Arabidopsis thaliana* seeds are

10    planted in commonly used planting pots and grown in an environmental chamber. After 5-6 weeks the plants are in the reproductive growth phase. Stems are bolting from the base of the plants. After 7 weeks, more stems and floral buds appear, and a few flowers are starting to open. Roots of 7-week old plants from pots are rinsed intensively with tap water to wash away dirt, and briefly blotted by paper towel to take away free water. The tissues are immediately frozen in

15    liquid nitrogen and stored at -80'C until total RNA extraction.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York

20    U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the

25    manufacturer.

The cDNA library of the present invention designated LIB24, is prepared from *Arabidopsis thaliana*, Columbia ecotype, flower bud tissue. Wild type *Arabidopsis thaliana*

seeds are planted in commonly used planting pots and grown in an environmental chamber. Flower buds are green and unopened and are harvested about seven weeks after planting. The tissue is immediately frozen in liquid nitrogen and stored at -80'C until total RNA extraction.

The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL,

5    Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

Construction of plant cDNA libraries is well-known in the art and a number of cloning

10    strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

The cDNA library of the present invention designated LIB25, is prepared from

15    *Arabidopsis thaliana*, Columbia ecotype, open flower tissue. Wild type *Arabidopsis thaliana* seeds are planted in commonly used planting pots and grown in an environmental chamber. Flower are completely opened with all parts of floral structure observable, but no siliques are appearing, and are harvested about seven weeks after planting. The tissue was immediately frozen in liquid nitrogen and stored at -80'C until total RNA extraction.

20    The stored RNA is purified using Trizol reagent from Life Technologies (Gibco BRL, Life Technologies, Gaithersburg, Maryland U.S.A.), essentially as recommended by the manufacturer. Poly A+ RNA (mRNA) is purified using magnetic oligo dT beads essentially as recommended by the manufacturer (Dynabeads, Dynal Corporation, Lake Success, New York U.S.A.).

25    Construction of plant cDNA libraries is well-known in the art and a number of cloning strategies exist. A number of cDNA library construction kits are commercially available. The Superscript™ Plasmid System for cDNA synthesis and Plasmid Cloning (Gibco BRL, Life

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Technologies, Gaithersburg, Maryland U.S.A.) is used, following the conditions suggested by the manufacturer.

## Example 3

### Detection of Changes in Sterol Metabolism

5      A labeled acetyl-CoA molecule, squalene molecule, or acetate are used in a variety of assays to detect changes in sterol production, secretion, localization, protein-binding, degradation, and trafficking known in the art. The example below illustrates.

Cells from transformed plants are cultured in an appropriate medium. Labeled acetate, preferably $^{14}$C-labeled, is added to a concentration of about 1 uCi/ml. After a period of growth,

10     the cells are collected, the lipids extracted, and resolved by thin-layer chromatography or run over HPLC column using known methods. The levels of each sterol resolved can be compared to control cells fed the same labeled $^{14}$C acetate and the amount of $^{14}$C-labeled sterol for each determined from the resolved sterols.

### References

15     In addition to those references cited and incorporated by reference above, the below references are incorporated in their entirety. In addition, these references, as well as each of those cited in the Summary and Detailed Description above, can be relied upon to make and use aspects of the invention.

Jiang, *et al.,* A new family of yeast genes implicated in ergosterol synthesis is related to the

20     human oxysterol-binding protein. *Yeast* 10: 341-53 (1994).

Fang, *et al.,* Kes1p shares homology with human oxysterol-binding protein and participates in a novel regulatory pathway for yeast Golgi-derived transport vesicle biogenesis. *EMBO J.* 15: 6447-59(1996).

Crowley, *et al.,* A mutation in a purported regulatory gene affects control of sterol uptake in

25     Saccharomyces cerevisiae. *Journal of Bacteriology,* 180(16): 4177-83 (1998).

Casperand Holt. Expression of the green fluorescent protein-encoding gene from a tobacco mosaic virus-based vector. *Gene* 173: 69-73 (1996).

**We claim:**

1. A substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 622.

5  2. The substantially purified nucleic acid molecule of claim 1, wherein the nucleic acid molecule comprises the nucleic acid sequence of SEQ ID NO: 1.

3. A substantially purified nucleic acid molecule that specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 1 or its complement, wherein the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO: 622.

10  4. The substantially purified nucleic acid molecule according to claim 3, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 1 or its complement under high stringency conditions.

5. The substantially purified nucleic acid molecule according to claim 3, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 1 or its

15  complement under low stringency conditions.

6. A substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 623.

7. The substantially purified nucleic acid molecule of claim 6, wherein the nucleic acid molecule comprises the nucleic acid sequence of SEQ ID NO: 2.

20  8. A substantially purified nucleic acid molecule that specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 2 or its complement, wherein the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO: 623.

9. The substantially purified nucleic acid molecule according to claim 8, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 2 or its

25  complement under high stringency conditions.

10.    The substantially purified nucleic acid molecule according to claim 8, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 2 or its complement under low stringency conditions.

11.    A substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 624.

12.    The substantially purified nucleic acid molecule of claim 11, wherein the nucleic acid molecule comprises the nucleic acid sequence of SEQ ID NO: 3.

13.    A substantially purified nucleic acid molecule that specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 3 or its complement, wherein the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO: 624.

14.    The substantially purified nucleic acid molecule according to claim 13, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 3 or its complement under high stringency conditions.

15.    The substantially purified nucleic acid molecule according to claim 13, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 3 or its complement under low stringency conditions.

16.    A substantially purified nucleic acid molecule that encodes a protein comprising the amino acid sequence of SEQ ID NO: 625.

17.    The substantially purified nucleic acid molecule of claim 16, wherein the nucleic acid molecule comprises the nucleic acid sequence of SEQ ID NO: 4.

18.    A substantially purified nucleic acid molecule that specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 4 or its complement, wherein the nucleic acid molecule encodes a protein comprising the amino acid sequence of SEQ ID NO: 625.

19.    The substantially purified nucleic acid molecule according to claim 18, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 4 or its complement under high stringency conditions.

20.    The substantially purified nucleic acid molecule according to claim 18, wherein said nucleic acid molecule specifically hybridizes to a nucleic acid sequence of SEQ ID NO: 4 or its complement under low stringency conditions.

21.    A substantially purified nucleic acid molecule comprising a nucleic acid sequence which

5    encodes a plant HES1 protein.

22.    A substantially purified protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 622, 623, 624, and 625.

23.    An antibody capable of specifically binding a protein with the amino acid sequence of SEQ ID NO: 622.

10    24.    An antibody capable of specifically binding a protein with the amino acid sequence of SEQ ID NO: 625.

25.    A transformed plant having a nucleic acid molecule which comprises:

(A)    an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule; which is linked to

15    (B)    a structural nucleic acid molecule, wherein said structural nucleic acid molecule comprises a nucleic acid sequence encoding a protein having an amino acid sequence selected from the group consisting of SEQ ID NO: 622 through SEQ ID NO: 626 or fragment thereof; which is linked to

(C)    a 3' non-translated sequence that functions in the plant cell to cause termination of

20    transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

26.    The transformed plant according to claim 25, wherein said structural gene is in the antisense orientation.

27.    The transformed plant according to claim 25, wherein said plant is selected from the

25    group of rapeseed, maize, soybean, safflower, sunflower, cotton, peanut, flax, oil palm and Cuphea.

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## Abstract

This invention relates to the field of biotechnology, particularly as it pertains to the

production of sterols in a variety of host systems particularly plants. More specifically, the

invention relates to nucleic acid molecules encoding proteins and fragments of proteins

5     associated with sterol and phytosterol synthesis and metabolism as well as the encoded proteins

and fragments of proteins and antibodies capable of binding to them. The invention also relates

to methods of using the nucleic acid molecules, fragments of the nucleic acid molecules,

proteins, and fragments of proteins. The invention also relates to cells, organisms, plants, or

seeds, or progeny of any, that have been manipulated to contain increased levels or overexpress

10    at least one sterol or phytosterol compound.

<110>     Karunanandaa, Balasulojini
          Yu, Jaehyuk
          Kishore, Ganesh M.

<120>     NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
          WITH STEROL SYNTHESIS AND METABOLISM

<130>     05686.0004.NPUS00

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<151>     1999-07-12

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Met Glu Tyr Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro
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Tyr Met Arg Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr
             30                  35                  40

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     60                  65                  70

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Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe
75                  80                  85                  90

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Thr Tyr Asp Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser
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His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
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Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg
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Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr
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Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly
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2

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gaaattaaag ttatcttcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc   1350

ggccgccg                                                           1358
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<210>      2
<211>      1136
<212>      DNA
<213>      Glycine max

<220>
<221>      CDS
<222>      (73)...(975)

<400>      2

gaattcggct cgaggtcaca acttcagtgc tatggtgaat cagtgtattg cacaggttcg      60

gacttgctaa gc atg tgc aac aat ggt cag agt cca ctt gat agg ttc ata      111
              Met Cys Asn Asn Gly Gln Ser Pro Leu Asp Arg Phe Ile
               1               5                  10

tct gtg gta gca tgg tgc ata tct acc act cgc cct gtg act ttt ggt      159
Ser Val Val Ala Trp Cys Ile Ser Thr Thr Arg Pro Val Thr Phe Gly
     15                  20                  25

gtt gct cct tat aat ccc att ctt ggt gag aca cac cat gtt tca agg      207
Val Ala Pro Tyr Asn Pro Ile Leu Gly Glu Thr His His Val Ser Arg
30                  35                  40                  45

gga aat ctt aat gtg tta ttg gag cag att tca cat cac cct cca gta      255
Gly Asn Leu Asn Val Leu Leu Glu Gln Ile Ser His His Pro Pro Val
                50                  55                  60

act gct ctc cat gca aca gat gag aag gaa aac att gaa atg tta tgg      303
Thr Ala Leu His Ala Thr Asp Glu Lys Glu Asn Ile Glu Met Leu Trp
            65                  70                  75
```

3

```
tgc cag cga cct gat cca aag ttt aat ggc aca tca gtt gaa gct aaa      351
Cys Gln Arg Pro Asp Pro Lys Phe Asn Gly Thr Ser Val Glu Ala Lys
        80                  85                  90

gtg cat gga ata cgc cag ttg aag ctc cta aat cat ggt gaa aca tat      399
Val His Gly Ile Arg Gln Leu Lys Leu Leu Asn His Gly Glu Thr Tyr
    95                 100                 105

gaa atg aat tgt cct cgc ctt tta ctt aga att ctt cca gtt cct ggt      447
Glu Met Asn Cys Pro Arg Leu Leu Leu Arg Ile Leu Pro Val Pro Gly
110                 115                 120                 125

gct gat tgg gct ggt aca gtt aat ata cgg tgc cta gag aca ggt cta      495
Ala Asp Trp Ala Gly Thr Val Asn Ile Arg Cys Leu Glu Thr Gly Leu
                130                 135                 140

gta gct gaa tta tcc tac aga tca agt tct ttt cta gga att ggg ggg      543
Val Ala Glu Leu Ser Tyr Arg Ser Ser Ser Phe Leu Gly Ile Gly Gly
            145                 150                 155

aat cat aga gtg atc aaa ggg aag atc ctt gac tct tca tca ttg aaa      591
Asn His Arg Val Ile Lys Gly Lys Ile Leu Asp Ser Ser Ser Leu Lys
            160                 165                 170

gtt cta tat gaa gtt gat ggt cat tgg gat agg acc gta aaa gtg aag      639
Val Leu Tyr Glu Val Asp Gly His Trp Asp Arg Thr Val Lys Val Lys
        175                 180                 185

gac aca aat aat ggg aaa gta aga gtg ata tat gat gca aag gaa gtt      687
Asp Thr Asn Asn Gly Lys Val Arg Val Ile Tyr Asp Ala Lys Glu Val
190                 195                 200                 205

atg tca ggt ctc gaa act cct ata ctc aag gac ata gag ggt gtg tgg      735
Met Ser Gly Leu Glu Thr Pro Ile Leu Lys Asp Ile Glu Gly Val Trp
                210                 215                 220

caa aca gaa tca gct cat gtt tgg ggt gaa tta aac caa gcc att gtg      783
Gln Thr Glu Ser Ala His Val Trp Gly Glu Leu Asn Gln Ala Ile Val
                225                 230                 235

agc aaa gac tgg gag aaa gca aga gaa gca aag cta aaa gtt gag gaa      831
Ser Lys Asp Trp Glu Lys Ala Arg Glu Ala Lys Leu Lys Val Glu Glu
            240                 245                 250

aga caa agg gag ctt gtg aga gaa aga gaa tca aaa gga gaa aca tgg      879
Arg Gln Arg Glu Leu Val Arg Glu Arg Glu Ser Lys Gly Glu Thr Trp
    255                 260                 265

att tct aag cat ttt gta gtt tct aac aac aaa gaa ggg tgg caa tgt      927
Ile Ser Lys His Phe Val Val Ser Asn Asn Lys Glu Gly Trp Gln Cys
270                 275                 280                 285

tca cct att cat aag agt gta cct gcg gcc ccc atc aca gcc cta taa      975
Ser Pro Ile His Lys Ser Val Pro Ala Ala Pro Ile Thr Ala Leu
```

4

ttgttgtcac tgtcaagtag tgtaaagcat taaagtacat tttagaagag aatgttcata    1035

aaaaaattta atggttgaaa ttttgacaac aatgaagtat ataacaaaat ttaaaattag    1095

ttacaatttt aaaaaaaaaa aaaaaaaaag ggcggccgcc g                        1136


<210>      3
<211>      1355
<212>      DNA
<213>      Glycine max

<220>
<221>      CDS
<222>      (32)...(1099)

<400>      3

ggaattcggc tcgaggacaa tgcttcagaa a atg gct gag ctt atg gag tac        52
                                    Met Ala Glu Leu Met Glu Tyr
                                     1               5

tct tac ctg tta gat atg gcg gac aag act gag gat cca tac atg aga       100
Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Met Arg
        10                  15                  20

cta gta tat gct tca tca ttc ttt ata tct gtc tac tat gcc tat caa       148
Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr Ala Tyr Gln
        25                  30                  35

cga acg tgg aag cca ttc aat cca att ctt ggt gag act tat gaa atg       196
Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met
40                  45                  50                  55

gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc agt cat cac       244
Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val Ser His His
                60                  65                  70

cct cca atg agt gct ggg cat gct gaa act gaa cat ttc act tat gat       292
Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe Thr Tyr Asp
                75                  80                  85

gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca gtt gat gta       340
Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Val Asp Val
            90                  95                  100

tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat ggt gtg gtc       388
Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val
        105                 110                 115

ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg att ttt gga       436
Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu Ile Phe Gly

5

```
cga act tgg att gat tca cca gga gag atg atc ctg aca aat ctg act      484
Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr Asn Leu Thr
                140                145                150

aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc tgg ttt gga      532
Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly
                155                160                165

gct ggt aga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag      580
Ala Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu
                170                175                180

cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa      628
Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln
                185                190                195

gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag      676
Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu
200                205                210                215

att tgg aga gtt gct gat acc ccg aag aag gac aag ttc cag tac acg      724
Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr
                220                225                230

cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg      772
His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
                235                240                245

ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag      820
Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys
                250                255                260

ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg      868
Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg
                265                270                275

caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act      916
Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr
280                285                290                295

cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt      964
Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly
                300                305                310

gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct      1012
Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala
                315                320                325

gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa      1060
Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu
                330                335                340
```

6

```
ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcatcct        1109
Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu
    345                 350                 355

tgtggaattc tttctatttt tttgaaatat cattttgtta ttaagtttgt aatgtaatct      1169

tgattggaat gcttgaaatt tggttttgtt tttgggttgt tttatcactg tagtatttga      1229

ttaattaata gtagctatgt tagttcatca gttcactttg catggataaa tgctagtaga      1289

gaaattaaag ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaagggcgg      1349

ccgccg                                                                 1355


<210>      4
<211>      1422
<212>      DNA
<213>      Zea mays

<220>
<221>      CDS
<222>      (1)...(1245)

<400>      4

atg gct acc aaa gaa gaa gct agc gct gtc ccc gcc gcc agt aaa act        48
Met Ala Thr Lys Glu Glu Ala Ser Ala Val Pro Ala Ala Ser Lys Thr
1                5                   10                  15

tca tgg agt agc ttc ctg aag tcc atc gca tcc ttc aac ggc gac ctc        96
Ser Trp Ser Ser Phe Leu Lys Ser Ile Ala Ser Phe Asn Gly Asp Leu
                20                  25                  30

tcc tct ctc acc gca ccg ccg ttc atc ctc tca aca acc tct tta acc       144
Ser Ser Leu Thr Ala Pro Pro Phe Ile Leu Ser Thr Thr Ser Leu Thr
            35                  40                  45

gag tat tct gcg tac tgg tgc gaa cat cct gca ctc ttc gtt gcc ccc       192
Glu Tyr Ser Ala Tyr Trp Cys Glu His Pro Ala Leu Phe Val Ala Pro
        50                  55                  60

gca cgt gag ccc gat cct gcg aag aga gcg ctc ttg gtg ctg aaa tgg       240
Ala Arg Glu Pro Asp Pro Ala Lys Arg Ala Leu Leu Val Leu Lys Trp
65                  70                  75                  80

ttc ctg agc aca ttg cac caa cag tac tgc tct cga agc gaa aag cta       288
Phe Leu Ser Thr Leu His Gln Gln Tyr Cys Ser Arg Ser Glu Lys Leu
                85                  90                  95

gga agc gag aaa aag ccg ctc aac ccg ttc ctg ggc gag ctt ttc ctg       336
Gly Ser Glu Lys Lys Pro Leu Asn Pro Phe Leu Gly Glu Leu Phe Leu
            100                 105                 110
```

7

```
ggc aag tgg ata gag gat gag gat gtg ggc gag aca agg ttg atc agc    384
Gly Lys Trp Ile Glu Asp Glu Asp Val Gly Glu Thr Arg Leu Ile Ser
        115             120             125

gag caa gtc agc cat cat cct cct gcg aca gcg tat tca ata gtc aat    432
Glu Gln Val Ser His His Pro Pro Ala Thr Ala Tyr Ser Ile Val Asn
    130             135             140

gag aaa cat gga gtt gag ctc caa gga tac aac gcc caa aaa gcc tcc    480
Glu Lys His Gly Val Glu Leu Gln Gly Tyr Asn Ala Gln Lys Ala Ser
145             150             155             160

ttc tcc agc acc atc caa gtg aaa caa cta ggc cac gcc tat ctc tcc    528
Phe Ser Ser Thr Ile Gln Val Lys Gln Leu Gly His Ala Tyr Leu Ser
                165             170             175

tta acg ccg ccc gga aaa gat gca aac aac gaa gac gac cgt gag cac    576
Leu Thr Pro Pro Gly Lys Asp Ala Asn Asn Glu Asp Asp Arg Glu His
            180             185             190

tac ctc atc acc ctc ccc aac ctc cac atc gaa tcc ctg atc tat ggg    624
Tyr Leu Ile Thr Leu Pro Asn Leu His Ile Glu Ser Leu Ile Tyr Gly
        195             200             205

aca cca ttc gtt gaa ttg gaa aag agt tgc aag atc gcc agc tca acc    672
Thr Pro Phe Val Glu Leu Glu Lys Ser Cys Lys Ile Ala Ser Ser Thr
    210             215             220

ggg tac atc tct aag ata gac ttt tcg ggc aaa ggc tgg ctg agc gga    720
Gly Tyr Ile Ser Lys Ile Asp Phe Ser Gly Lys Gly Trp Leu Ser Gly
225             230             235             240

aag aaa aat acc ttc tcc gca gtg tta tac aag gaa agc gac ggc gaa    768
Lys Lys Asn Thr Phe Ser Ala Val Leu Tyr Lys Glu Ser Asp Gly Glu
                245             250             255                 .

aaa aat cct tta tac aca gcc gac ggt caa tgg tcg agc agc ttc act    816
Lys Asn Pro Leu Tyr Thr Ala Asp Gly Gln Trp Ser Ser Ser Phe Thr
            260             265             270

atc cgc gat gca cgc gct aag aag gat att gag acc ttc act atc agc    864
Ile Arg Asp Ala Arg Ala Lys Lys Asp Ile Glu Thr Phe Thr Ile Ser
        275             280             285

aat ctg aaa aca acc ccc tta aca gtc gcc cct ctt gat gaa caa gat    912
Asn Leu Lys Thr Thr Pro Leu Thr Val Ala Pro Leu Asp Glu Gln Asp
    290             295             300

gaa tgg gaa act cgc cgt gca tgg cgc gac gta gca gcc gcc atc gaa    960
Glu Trp Glu Thr Arg Arg Ala Trp Arg Asp Val Ala Ala Ala Ile Glu
305             310             315             320

cgc ggc gac atg gaa gcc aca tca aac gcc aaa acc aag atc gaa gtc   1008
Arg Gly Asp Met Glu Ala Thr Ser Asn Ala Lys Thr Lys Ile Glu Val
```

8

```
gcg caa cga gaa ctc cgc aaa aag gag aaa gag caa ggc gag gag tgg    1056
Ala Gln Arg Glu Leu Arg Lys Lys Glu Lys Glu Gln Gly Glu Glu Trp
        340                  345                  350

gaa cga cga ttc ttc aag cga gtc aac gaa aag gat gaa cct acc ttt    1104
Glu Arg Arg Phe Phe Lys Arg Val Asn Glu Lys Asp Glu Pro Thr Phe
        355                  360                  365

atg aga ttg gcg gcg atg ctg gat ttg acg caa ggc atc gaa agt gac    1152
Met Arg Leu Ala Ala Met Leu Asp Leu Thr Gln Gly Ile Glu Ser Asp
    370                  375                  380

cgc acc ggg gga gtt tgg agg ttt gat cct tca cgt gct gtg gat gcg    1200
Arg Thr Gly Gly Val Trp Arg Phe Asp Pro Ser Arg Ala Val Asp Ala
385                  390                  395                  400

aat ccg ccg tat cac aag gtt ggc ggc gaa ggg ttg gga ttg taa        1245
Asn Pro Pro Tyr His Lys Val Gly Gly Glu Gly Leu Gly Leu
                405                  410
```

```
tttatttatg aggcatcttt tatatttcat aaaaacaggg tctaggccgt ttattcatta    1305

aatgtgtatt aagtagcgct ttttctcgac cgttgagatt catggatgca agtgtaccta    1365

atagctcaat gcgagactct ttccaagcaa aaaaaaaaaa aaaaaaaggg cggccgc       1422
```

```
<210>      5
<211>      2126
<212>      DNA
<213>      Saccharomyces cerevisiae

<220>
<221>      CDS
<222>      (453)...(1757)

<400>      5

aacctctccg cccgtatatt ttttttaata tgttaaatag tgatagaact gataagcctc    60

attttctttt attgggctcc aagacgcgaa ctgttcgtag ggtaaccgtt tgacacctaa    120

acgacctttc agcctcacct gcagtatttc ttcaacaacg cctgtcgcta tgttaaataa    180

tagcaatcgt ttgtgatcac cattgtcgaa tttgacgcgc ttaaacaaaa accattgttt    240

tggcctcgtt ccctgcattc aacaaagag caaggtatgc cgtcaaacag tcgttaaaag    300

agaaggttta taaactatct tgttttgtac tttgctgtcc cggatccagt tgggtcttct    360

tttcaacctg tctgagtccg atctttcttt ccctacttga agctccatat atctaagtca    420
```

9

```
tctaagtgta tcctgctaga ttacaaacga aa atg tct caa cac gca agc tca        473
                                    Met Ser Gln His Ala Ser Ser
                                    1           5


tct tct tgg act tct ttt ttg aaa tcg ata agt tcg ttc aac gga gat        521
Ser Ser Trp Thr Ser Phe Leu Lys Ser Ile Ser Ser Phe Asn Gly Asp
        10              15                  20


cta tcg tct ttg tct gca cca ccg ttt att ctt tct ccc act tcc tta        569
Leu Ser Ser Leu Ser Ala Pro Pro Phe Ile Leu Ser Pro Thr Ser Leu
    25              30                  35


aca gag ttt tct cag tat tgg gct gaa cat cca gct tta ttt ctg gag        617
Thr Glu Phe Ser Gln Tyr Trp Ala Glu His Pro Ala Leu Phe Leu Glu
40              45                  50                  55


cct tcg ttg att gat ggt gaa aac tac aaa gat cac tgt ccc ttt gac        665
Pro Ser Leu Ile Asp Gly Glu Asn Tyr Lys Asp His Cys Pro Phe Asp
                60                  65                  70


cca aat gtg gaa tca aag gaa gtg gcg cag atg ttg gcg gtt gtt agg        713
Pro Asn Val Glu Ser Lys Glu Val Ala Gln Met Leu Ala Val Val Arg
                75                  80                  85


tgg ttt att tct act ttg aga tct caa tac tgc tct aga agc gaa tcg        761
Trp Phe Ile Ser Thr Leu Arg Ser Gln Tyr Cys Ser Arg Ser Glu Ser
            90                  95                  100


atg ggt tct gaa aag aag cct ttg aac cca ttc ttg ggt gag gta ttt        809
Met Gly Ser Glu Lys Lys Pro Leu Asn Pro Phe Leu Gly Glu Val Phe
    105                 110                 115


gtt gga aag tgg aaa aat gat gag cat cca gag ttt ggt gaa acg gtt        857
Val Gly Lys Trp Lys Asn Asp Glu His Pro Glu Phe Gly Glu Thr Val
120                 125                 130                 135


ctt tta agt gag caa gtt tca cat cat cca cct atg aca gca ttt tcg        905
Leu Leu Ser Glu Gln Val Ser His His Pro Pro Met Thr Ala Phe Ser
                140                 145                 150


att ttt aat gaa aaa aat gat gtt tct gtt caa gga tac aat caa att        953
Ile Phe Asn Glu Lys Asn Asp Val Ser Val Gln Gly Tyr Asn Gln Ile
                155                 160                 165


aaa act ggt ttt acc aaa aca ttg acg cta acg gtc aaa cca tac ggg        1001
Lys Thr Gly Phe Thr Lys Thr Leu Thr Leu Thr Val Lys Pro Tyr Gly
            170                 175                 180


cat gtc att ttg aag att aaa gat gag acc tac ctg att aca acc ccg        1049
His Val Ile Leu Lys Ile Lys Asp Glu Thr Tyr Leu Ile Thr Thr Pro
    185                 190                 195


cct ttg cat atc gaa ggt att tta gtc gct tct cca ttt gtt gaa tta        1097
Pro Leu His Ile Glu Gly Ile Leu Val Ala Ser Pro Phe Val Glu Leu
```

10

```
gga ggc agg tca ttc ata cag tca tca aat ggt atg tta tgt gtt ata   1145
Gly Gly Arg Ser Phe Ile Gln Ser Ser Asn Gly Met Leu Cys Val Ile
                220                    225                    230

gaa ttt tca gga agg ggg tat ttc aca ggg aag aag aac tcc ttt aag   1193
Glu Phe Ser Gly Arg Gly Tyr Phe Thr Gly Lys Lys Asn Ser Phe Lys
                235                    240                    245

gca aga att tac aga agc cca caa gag cat agt cat aaa gaa aat gcg   1241
Ala Arg Ile Tyr Arg Ser Pro Gln Glu His Ser His Lys Glu Asn Ala
                250                    255                    260

cta tac cta atc tct ggc caa tgg tca ggt gtt tca aca att ata aaa   1289
Leu Tyr Leu Ile Ser Gly Gln Trp Ser Gly Val Ser Thr Ile Ile Lys
                265                    270                    275

aaa gac tcg caa gtt tca cat cag ttt tac gat tca tcg gaa act cct   1337
Lys Asp Ser Gln Val Ser His Gln Phe Tyr Asp Ser Ser Glu Thr Pro
280                    285                    290                    295

act gaa cat tta tta gtt aag cca atc gaa gaa caa cat cct ctg gaa   1385
Thr Glu His Leu Leu Val Lys Pro Ile Glu Glu Gln His Pro Leu Glu
                300                    305                    310

agt agg agg gca tgg aag gat gtg gca gaa gca atc aga caa gga aat   1433
Ser Arg Arg Ala Trp Lys Asp Val Ala Glu Ala Ile Arg Gln Gly Asn
                315                    320                    325

att agt atg ata aaa aag act aag gaa gaa cta gaa aat aag caa aga   1481
Ile Ser Met Ile Lys Lys Thr Lys Glu Glu Leu Glu Asn Lys Gln Arg
                330                    335                    340

gcc ttg aga gaa caa gaa cgc gta aaa ggt gtg gaa tgg caa aga aga   1529
Ala Leu Arg Glu Gln Glu Arg Val Lys Gly Val Glu Trp Gln Arg Arg
                345                    350                    355

tgg ttc aaa caa gtg gac tac atg aat gaa aat aca tca aat gat gta   1577
Trp Phe Lys Gln Val Asp Tyr Met Asn Glu Asn Thr Ser Asn Asp Val
360                    365                    370                    375

gag aaa gca agt gaa gat gat gcc ttt agg aaa ttg gcg tcc aaa ctg   1625
Glu Lys Ala Ser Glu Asp Asp Ala Phe Arg Lys Leu Ala Ser Lys Leu
                380                    385                    390

cag ctt tct gtg aaa aat gtg cca agt ggg aca ttg att ggc ggc aaa   1673
Gln Leu Ser Val Lys Asn Val Pro Ser Gly Thr Leu Ile Gly Gly Lys
                395                    400                    405

gat gat aag aaa gat gtt tca acc gca ttg cat tgg agg ttt gat aaa   1721
Asp Asp Lys Lys Asp Val Ser Thr Ala Leu His Trp Arg Phe Asp Lys
                410                    415                    420
```

aat ttg tgg atg agg gag aac gaa att act ata taa tataaatgtt          1767
Asn Leu Trp Met Arg Glu Asn Glu Ile Thr Ile
    425                 430


tttaaaagaa taaatatcaa aaattaatac taattgatgt ttgcattgct tttttttaagg    1827

gaaaatgcaa gcgtttttat ttttaacttt tggtttttgaa gctcgtaatt caacaaaaaa    1887

gaattaaata atcttcaagt ccgataacaa gatgtagaaa aaacatccca atgaagttac    1947

aagtcaaacc attcactgag aattttttgta actcaccacc gattttttgg ataaaatgta    2007

ttcctgcaac tttttttttt gaagagataa aaagaattga atagaatatg cagtaaaaaa    2067

agaatctcga aaaaaaaagg acaagaaatc ttaactacca tcaaacaatt gaaaattga    2126


<210>          6
<211>          266
<212>          DNA
<213>          Glycine max

<400>          6

ccattcaatc caattcttgg tgagacttat gaaatggtta accatggtgg cattacattt      60

atatcagagc aggtcagtca tcaccctcca atgagtgctg ggcatgctga aactgaacat    120

ttcacttatg atgttacatc aaaattgaaa accaaatttc tcggcaactc agttgatgta    180

tatcctgttg gaagaacgcg tgttaccctc aaaagagatg gtgtggtcct tgatttggtg    240

cctcctccta caaaagttag caactt                                          266


<210>          7
<211>          291
<212>          DNA
<213>          Glycine max

<220>
<223>          unsure at all n locations

<400>          7

tcacaacttc agtgctatgg tgaatcagtg tattgcacag gttcggactt gctaagcatg      60

tgcaacaatg gtcagagtcc acttgatagg ttcatatctg tggtagcatg gtgcatatct    120

accactcgcc ctgtgacttt tggtgttgct ccttataatc ccantcttgg tgagacacac    180

cncgtttcaa ggggaaatct taatgtgtta ttggagcaga tttcacatca ccctccagta    240

actgctctcc atgcaacaga tgaganggaa aacattgaaa tgttatggtg c             291


12

```
<210>      8
<211>      282
<212>      DNA
<213>      Glycine max

<220>
<223>      unsure at all n locations

<400>      8

gtgcccagng acaggtctgg tagctgaaat atcatacatg atcaagccat tgcttttta    60

ggatttnggg gaagtcgtaa attgatcaaa gggnaaatcc ttgactcatn attactcaaa   120

ggtctctgcg aagttgatng tcattgggat aagatagtta gagtgaagga tacnaatagt   180

gnagaagtga gagtgatata tgatgccaaa gaagccnttt caggtctcaa aactcctatt   240

atcaaggatg tggagagtgt gtggccaacc gaatcagccc tt                      282


<210>      9
<211>      255
<212>      DNA
<213>      Glycine max

<400>      9

gtaactccta cccccttgggg tgacttggaa gtttaccaat acaacggtaa atatacccaa   60

cattgtgctg ccgttgatag ttctgagtgc attgaagtgc ctgacatcag accagaattc   120

aacccttggc aatatgataa tttggatgct gaatagtgag catccttgtg gaattctttc   180

tattttttt aaatatcatt ttgttattaa gtttgtaatg taatcttgat tggaagcttg     240

aaatttggtt ttgtt                                                    255


<210>      10
<211>      250
<212>      DNA
<213>      Glycine max

<400>      10

taactcctac cccttggggt gacttggaag tttaccaata caacggtaaa tatacccaac    60

attgtgctgc cgttgatagt tctgagtgca ttgaagtgcc tgacatcaga ccagaattca   120

acccttggca atatgataat ttggatgctg aatagtgagc atccttgtgg aattctttct   180
```

13

atttttttta aatatcattt tgttattaag tttgtaatgt aatcttgatt ggaatgcttg    240

aaatttggtt                                                            250


<210>      11
<211>      283
<212>      DNA
<213>      Glycine max

<220>
<223>      unsure at all n locations

<400>      11

cgcctgtgnt taatttccca aaatctcaac ttcaatgcta nggtgaatca gtgtactgca     60

catcttccaa cttgctaagc caatgcaaac agtgggcaga gtccactgga caggttcaca    120

tcagtagtag catggagcat atctaccaca cgccccacat cttttggtgt tgctccttat    180

aattccactc ttggagagac ccaccatgtt tccaagggca atctcaacgt cctagttgag    240

caggtttcac tcaatcctcc agtatctgcc ctccatgcaa cag                     283


<210>      12
<211>      255
<212>      DNA
<213>      Glycine max

<400>      12

ggagagtgtg tggccaaccg aatcagccct tgtttggagt gagttgagcc aagccattat     60

gaacaaagat tgggaaagag caagagaagc aaagcaagac gtggaagaaa gacagaggaa    120

tatgttgaga gacagagcca tgaaaggaga aacttggttt cctaagaatt ttagggtgtc    180

ttacagtaaa gacacatggg aatgggactg ttcaccaact cataaatggg tccctgaggc    240

ccccatcata gctca                                                     255


<210>      13
<211>      259
<212>      DNA
<213>      Glycine max

<220>
<223>      unsure at all n locations

<400>      13


14

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agtcaaccct ccagtatctg ccctccatgc aacagatgag anggaaaaca ttgagatgat   60

atggtcccag caacctgttc caaagtttcg gggtacatct atgaagctca agtgcatggt  120

aaacgtcata tgtttctcca tgatttagga gcttcagctg acgtttacca tgcacttgag  180

ctgangctcc taaatcatgg agaaacatat gaaatgaatt gtcctcacct ttcaattaga  240

attcttccgg ttcctggga                                                259



<210>      14
<211>      355
<212>      DNA
<213>      Glycine max

<220>
<223>      unsure at all n locations

<400>      14

gcagcttttg ctgtgtctag ctatgcgtca actgaangtc gacaatgtaa acctttaat    60

cctttactcg gggagaccta cgaagctgac tatccagata aaggacttaa gttttttct   120

gaaaaggtta gtcatcatcc aatgattgtt gcttgtcact gtgagggaag gggatggaag  180

ttttgggcag attctaattt gaaaggaaaa ttctgggggc gttctatcca gttagatcct  240

gtgggtgtcc tcactctaca gtttgaggat ggtgaaacat ttcagtggag caaggtcacc  300

acttcgattt acaatatcat actangtaaa atttattgtg accactacgg tacca         355



<210>      15
<211>      279
<212>      DNA
<213>      Glycine max

<220>
<223>      unsure at all n locations

<400>      15

cagattcgga ggaggaagct cagagaggaa gatggaaaca ggaggaaaga gatggttact   60

ggaagatgat gcagaagtat attggctcgg atgtaacatc aatggtgaca ctaccagtta  120

ttatatttga accaatgact atgattcaga aaattgctga gttgatggag tactcctact  180

tgttagatca agcagatgaa tcagaggatc catacatgca gttagtttat gcaatggatg  240

tacttnatgt atcatcacag catccatggg ccatatcgg                          279
```

```
<210>        16
<211>        191
<212>        DNA
<213>        Glycine max

<400>        16

gttgatagtt  ctgagtgcat  agaggtgcct  gacagcagaa  cagaattcaa  cccttggcaa     60

tatgataatt  tggatgctga  ataataagca  tccttgtaga  attctttcta  ttctttgaac    120

tatcattttg  ttattaagtt  tgcaatgtat  ctgattggaa  tgcttgaaat  ttggttttgt    180

ttttgggtaa  a                                                             191


<210>        17
<211>        267
<212>        DNA
<213>        Glycine max

<220>
<223>        unsure at all n locations

<400>        17

tcaactcctt  ggggtgattt  ggaaatctat  caatataatg  gtaaatacag  tgaacatcga     60

gctgctgcag  ataactcagg  aagcattgat  gatgttgatg  ctaaatcaat  tgaattcaat    120

ccatggcagt  atggtaattt  ggccacggaa  tgaactagtt  tcaatttctt  tggttttgga    180

tgntncagtt  agttcatgta  actnttnncn  antganacna  gaanacaact  ncctncnnca    240

ncnnanngtt  agttgggcng  tgtacgc                                           267


<210>        18
<211>        252
<212>        DNA
<213>        Glycine max

<400>        18

gtcttataga  gctcccaatc  tcctacatcg  cttgttaagt  ttactcaaga  acgtgcggcc     60

aggatcagat  ctcacacact  tccaactgcc  agctgtgttt  aacttcccaa  aatctcaact    120

tcaatgctat  ggtgaatcag  tgtactgcac  atcttcaaac  ttgctgagca  aatgcaacaa    180

tgggcagagt  ccactggaca  ggttcacatc  agtagtagca  tggagcatat  ctaccacacg    240

ccccacatct  tt                                                           252
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16

```
<210>      19
<211>      241
<212>      DNA
<213>      Glycine max

<400>      19

gtcagtcatc accctccaat gagtgctggg catgctgaaa ctgaacattt cacttatgat   60

gttacatcaa aattgaaaac caaatttctc ggcaactcag ttgatgtata tcctgttgga  120

agaacgcgtg ttaccctcaa aagagatggt gtggtccttg atttggtgcc tcctcctaca  180

aaagttagca acttgatttt tggacgaact tggattgatt caccaggaga gatgatcctg  240

a                                                                   241


<210>      20
<211>      262
<212>      DNA
<213>      Glycine max

<400>      20

tctcgagcct attcggctcg aggccaaaga agccatttca ggtcactaaa ctcctattat   60

catatgatgt ggagagtgtg tattcaaccg aatcagccct tgtttggagt gagttgagcc  120

aagccattat gaacaaagat tgggaaagag caagagaagc aaagcaagac gtggaagaaa  180

gacagaggaa tatgttgaga gacagagcca tgacaggaga aactggttgt ctaagaattt  240

agggtgtctt acagtaaaga ca                                            262


<210>      21
<211>      463
<212>      DNA
<213>      Arabidopsis thaliana

<220>
<223>      unsure at all n locations

<400>      21

ggggaacccc ttccaggaac agagctgaaa gaggtgtggc atttggctga tgtccccaaa   60

aacgacaact ttcagtacac tcactttgct cacaagataa acagcttcga cacagcgcct  120

gctaagctct tggcttcaga ctcacgtatc cgtcctgata gatattccct tgagcagggt  180
```

gacctttcta aagctggttc cgagaaacac agccttgagg agagacaaag ggccgaaaag 240

aggaccagag agacaaaggg acaaaagttc actccaagat ggttcgatct aacggatgag 300

atcacaccta ctccatgggg agatattgaa gtataccant acaacgggaa gtacaatgaa 360

caccgagaca cggcagagag ctcaagtagt gcctccaacg aaacgggact caaatccatc 420

gagtttaatc cttggcaata tggtaatatc tcaaccgaat gaa 463


<210>      22
<211>      399
<212>      DNA
<213>      Arabidopsis thaliana

<400>      22

agtgaacctc tcccaggcac cgaactgaaa gaggtatgga aactcgctga tgtgccaaag 60

gatgacaaat atcaatacac tcactttgct cacaagatta atagcttcga cactgccccg 120

aaaaagctgt tgccctctga ttcacggtta cgacctgata gatacgcact tgagatgggc 180

gacatgtcca aatcaggcta tgagaagagc agcatggaag agagacagag agctgacaag 240

agaacccgcg aacataaagg ccaagccttt actccaaaat ggttcgatgt aacggaagaa 300

gtcactgcta caccatgggg tgatctggaa gtttaccaat tcactggaaa gtactcagaa 360

catcgtgcag ctgcggataa ctctgaagat aagaccgac 399


<210>      23
<211>      343
<212>      DNA
<213>      Arabidopsis thaliana

<400>      23

acggacgcgt gggcaactcc aatgttacgg cgagatggtc tacagcttcg tcggtcagga 60

tctgcttggg gaatgcagcc gccgtgatct tcccattgaa cggctcaaat cagtggtgac 120

gtggaacatc tccacactcc gtccggtggt ctttggcatg tctccgtaca actccgttct 180

cggcgagact caccacgtat cgaacggtca catcaacgtc atcgccgaac aagtagtgca 240

tcatcctccg gtttccgctc ttcatgcgac tcacgaacaa gaaaatatcg acgtgacatg 300

gtgtcaatat ttcactccta aatttcgtgg tactcacgtg gac 343


<210>      24

18

<211>    510
<212>    DNA
<213>    Arabidopsis thaliana

<220>
<223>    unsure at all n locations

<400>    24

gaaagctagc agatgtagaa caaagttttt tgtaactacg agagaataag aatacatttg    60

tttccaaaaa gatttgatct tttctgtctt ttggagcgat acatttaagt agacagatct   120

tggaattgcc atgggttgaa ttggatcgac ttagggtcgg tgttatcttc agagttatcc   180

gcagctgcac gatgttccga gtactttcca ttgaattggt aaacttccag atcaccccat   240

ggtgtagcag tgacttcttc cgttacatcg aaccattttg gagtaaaggc ttggcctttc   300

tcttcgcggg gtcncttttc aagtctctgt cnctcttcca tggtgntctt cccanagcct   360

gatttgnaca tggcggccan cccaggggng gatcaatcag gccgnaacgg ggaatcagnn   420

ggnaacagct tttcngggna ntgncgaagc aataaaccnt ggggcaaag gggggggatt   480

ggaaattggc aacccttggn naacaggggc                                     510


<210>    25
<211>    282
<212>    DNA
<213>    Arabidopsis thaliana

<220>
<223>    unsure at all n locations

<400>    25

gatacatttg gattcgaaaa gagcagccta gaggatagac aaagagctga gaagaaaagc    60

agagaagaga aaggccaaaa ntttccncca aaatggtttn atgaaacana agangtcact   120

cctacaccat ggggtgatct cgaagtttac caattcantg gaaagtactc ggtgcaccgn   180

gccacagctg aaaactntga ggatacaacc gntgtgaagt tgncccaatt caacccttgg   240

caattccaag atctctntgc ttaatccttt ggtgccattt gt                      282


<210>    26
<211>    380
<212>    DNA
<213>    Arabidopsis thaliana

19

<220>
<223>      unsure at all n locations

<400>      26

cgttggtggc ngcggaagtg gtttcttcgc ctctcttgct tcgtcgatct ccaatttngg      60

ntctgctatg accaaatcag ttaatggttt ggttccctat gagggacttg aagttatcaa     120

tcctgaagga agtacagatg atgctgagga ggaagcaagc agaggaagat ggaagcaaga     180

ggatcgagat ggctattgga agatgatgca gaagtacata ggatctgatg ttacatcaat     240

ggtgaccctt cctgtgatta tttttgaacc aatgacaatg cttcagaaaa tggcggagtt     300

gatggaatac tcgcatctgc tagacatggc agacaaaacc gaggaccctt atttncgcat     360

ggtgtatgca tcatcgtggg                                                 380


<210>      27
<211>      359
<212>      DNA
<213>      Arabidopsis thaliana

<220>
<223>      unsure at all n locations

<400>      27

ggtaatgaag gagttgaggt cataaatcca gaaggtggca aggaagatnc tgaagaggaa      60

gctcagaaag gaaggtggaa ggacgaggaa cgagatagtt actggaagat gatgcagaaa     120

tatataggtt cggatattac gtcaatggtg gctcttcctg ttgtnatatt tnancctatg     180

actatnctcc anaagatggc tgagataatg gagtattctc atttnttgga tcaagcagat     240

gaatgcngag atccatactt gctgttagta tatccttcat catggggtat atctgtttac     300

tatggccttc caacggacct tggaagcctt tnaatccnat tcttgggggg gnnanttna     359


<210>      28
<211>      510
<212>      DNA
<213>      Arabidopsis thaliana

<220>
<223>      unsure at all n locations

<400>      28

aaaagagaaa agtgttagcc tttggtcaat gatcaaagac antataggga aggntctcac      60

20

```
aaaagtctgt cttcctgttt acttcaacga gccactttct tctttacaga aatgttttga    120

ggatttggaa tattcgtacc ttcttgaccg agcatttgaa tatggcaaaa ggggaaatag    180

cctcatgagg atacttaatg tagctgcttt tgctgtatct gggtatgcat caactgaagg    240

aagaatttgc aaacctttta atccattgtt aggtgaaaca tacgnggcag actatccaga    300

caaaggcctt cggttttttt ccaggaaagg tcagtcatca tcctatggtt gtcgnatgcc    360

attgtgatgg caccnggtgg gaattcttgg gggacagcaa tcttnggggc aaattttggg    420

gcgntctntt tagcttnacc cccttgggga ttnnccttna aattnatgat ggggaanccn    480

cagggggggaa ggngcccacc atnncaaacc                                    510
```

<210> 29
<211> 493
<212> DNA
<213> Arabidopsis thaliana

<220>
<223> unsure at all n locations

<400> 29

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cccncccng aaagnttccc ctgtttccgg nttnncccnt ntgnnccccc ttggggggggn     60

cctttcccaa tnggnnttgg gngngcccc ttggangggg ccggggcttt aaagggcccc    120

ncgnagggaa ggccagcctt tctcccaaat ggtcgatgta ccggaggaag tcactgctac    180

cccatggggt gatctggaag tttcccaatt caatggaaag tactcggaac atcgtgcagc    240

tgcggataac tctgaagata acaccgaccc taagtcgatc caattcaacc catggcaatt    300

ccaagatctg tctacttaaa tgtatcgctc caaaagacag aaaagatcaa atctttttgg    360

aaacaaatgt attcttattc tctcgtagtt acaaaaaact ttgttctaca tctgctagct    420

ttcccattgc tttctctagt attagtgtac aacttctact gttttgtctt aaattcattc    480

aaatctttct ttg                                                       493
```

<210> 30
<211> 1305
<212> DNA
<213> Saccharomyces cerevisiae

<400> 30

21

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atgtctcaac acgcaagctc atcttcttgg acttcttttt tgaaatcgat aagttcgttc    60

aacggagatc tatcgtcttt gtctgcacca ccgtttattc tttctcccac ttccttaaca   120

gagttttctc agtattgggc tgaacatcca gctttatttc tggagccttc gttgattgat   180

ggtgaaaact acaaagatca ctgtcccttt gacccaaatg tggaatcaaa ggaagtggcg   240

cagatgttgg cggttgttag gtggtttatt tctactttga gatctcaata ctgctctaga   300

agcgaatcga tgggttctga aaagaagcct ttgaacccat tcttgggtga ggtatttgtt   360

ggaaagtgga aaatgatga gcatccagag tttggtgaaa cggttctttt aagtgagcaa   420

gtttcacatc atccacctat gacagcattt tcgatttta atgaaaaaaa tgatgtttct   480

gttcaaggat acaatcaaat taaaactggt tttaccaaaa cattgacgct aacggtcaaa   540

ccatacgggc atgtcatttt gaagattaaa gatgagacct acctgattac aaccccgcct   600

ttgcatatcg aaggtatttt agtcgcttct ccatttgttg aattaggagg caggtcattc   660

atacagtcat caaatggtat gttatgtgtt atagaatttt caggaagggg gtatttcaca   720

gggaagaaga actcctttaa ggcaagaatt tacagaagcc cacaagagca tagtcataaa   780

gaaaatgcgc tatacctaat ctctggccaa tggtcaggtg tttcaacaat tataaaaaaa   840

gactcgcaag tttcacatca gttttacgat tcatcggaaa ctcctactga acatttatta   900

gttaagccaa tcgaagaaca acatcctctg gaaagtagga gggcatggaa ggatgtggca   960

gaagcaatca gacaaggaaa tattagtatg ataaaaaaga ctaaggaaga actagaaaat  1020

aagcaaagag ccttgagaga acaagaacgc gtaaaaggtg tggaatggca aagaagatgg  1080

ttcaaacaag tggactacat gaatgaaaat acatcaaatg atgtagagaa agcaagtgaa  1140

gatgatgcct ttaggaaatt ggcgtccaaa ctgcagcttt ctgtgaaaaa tgtgccaagt  1200

gggacattga ttggcggcaa agatgataag aaagatgttt caaccgcatt gcattggagg  1260

tttgataaaa atttgtggat gagggagaac gaaattacta tataa              1305


<210>      31
<211>      1200
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      31

atgacagtct cacacaatca ttctacgaag atatcccaac aaccaatctc ctcggtatca    60
```

22

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gcatttaagt tcttcggaaa gaagctgtta agttcaagcc atgggaacaa gttgaagaaa    120

aaggcgtctc tacctccaga cttccactct acaagtacta atgacagcga atcctccagc    180

ccaaaactgc cgaattcgtt gaaaacctct cgccgtgcaa actctttcgc tcacacaacc    240

aacagcaaga gatctttatc ttccgcctca accaagatcc tacctccggc cggctccagc    300

acgtccatct caagaggaaa cagacattcg tccacttcgc gtaatctctc aaactccaag    360

ttcagtagcg aacgattagt gtacaatcca tacggcgtct caaccccaag cacgtcactc    420

tcgtccgtct ctacctccat gaagaaagac cctgatctgg cttctacct tcacgatggg    480

gattccaaaa tccgcatgct gccgatccca attgtggacc caaacgagta tctgcccgac    540

gagatgaagg aggcaagcat ccagttgagc gataacttcg tctttgatga tgagaataag    600

accatcggat ggggcggttc gtgcgaagtg cgcaagatcc gctccaagta ccgcaagaag    660

gacgtatttg ctctaaagaa gctcaatatg atctataatg aaacgcccga gaaattctac    720

aacgctgctc caaaggagtt tatcatcgca aagcagctaa gtcatcatgt tcacatcaca    780

aatactttcc ttctagtcaa ggtgcccacc accgtctaca ccactcgcgg gtggggggttc    840

gtcatggagc taggtctacg agatttgttc gcgatgatac aaaaatcggg ctggcgccac    900

gtggccctag cagaaaagtt ttgtatattc aaacaggtgg cgtgtggtgt caagttttgc    960

cacgatcagg gcatcgccca ccgtgatttg aaaccggaaa atgtactgct atccccggac   1020

ggcgtgtgca agctgacaga ttttggtatc tcagactggt accaccacgg atccacacga   1080

cctgtccagc cctgtcaaga agtgcgcagg gatgatcggc tcgccgccgt atgctccccc   1140

ggaggtcatg ttctacgact ccaagaagca ctacgatacg gaattgcaac agccgtatga   1200


<210>        32
<211>        309
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        32

atggatcatc cacataagtg gcaccgtaag ctcgtcaatt gcaacagcga ctttattttt     60

aagagccgcg gtcattttgt tagtatctct tctcaacttg ggcagcacaa tttcacgata    120

tttaacaggt atcatttgaa aaaaagaatc gttttccaga tactcgtcaa ttcctcgctt    180

cggttctctg aacaaaactt ctcgattacg caaaatgagg ctggcatatg gaagcagttg    240
```

23

ttcaactctc cccaaagttt tccacatact gatataccat cagaagaagg taccaaagtt  300

attctataa                                                        309


<210>      33
<211>      4014
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      33

atggagcaca gatataacgt gtttaatgat actccacgag ggaaccattg gatgggcagt    60

tctgtgtcag gatcaccacg tccatcttat agcagtcgtc ctaatgtaaa cacaacacga   120

cgcttccaat atagtgacga tgagcccgct gagaaaatcc gacctttacg ctcgaggagc   180

tttaaaagta ctgaaagtaa cataagcgat gaaaaatcaa ggatatctga cgtgacagc    240

aaagaccgct acattaatgg tgataaaaag gtagacattt attcactgcc tctaatatca   300

accgatgttt tagaaatttc caaacaaagg acatttgcgg tgatattgtt tttaataatt   360

caatgttata aaatatatga cctggtaata cttaaatcgg ggttaccgct ttcgggttta   420

ctgtttaaga actatcgatt taatttcata tccaagtatt tcattataga ttccttcttc   480

ctgtatgttt taccatcctt taacattcct aggttgactt ttaagccatg ggttgtttat   540

ctccagattt tagctatgct actattgaac attttcatat caagcgatca cgagttcgtt   600

ttgatttcat taattatgac cacatggaga aaactttata cgaaagaatt aagtgtaaca   660

ggttcagcca ttaaccatca tcgtattttt gattcttccg ctcattttaa gggtgctcta   720

acaatcaaga tcctacctga aaacacagct atgtttaatc ctcttcatga atcatattgt   780

ttgcccatgg ataccaatct ttttaaaatt aactcaattg acgtacccat cagaataaac   840

tcaactgaag agattgaata tatcgagttg gaatatagag atctttacac aaattcggta   900

gagttacggt ctttgagtaa gaaagacttc aaaatcatcg ataaccccaa atcctttta   960

aaaaaagatc agtcagttct aaagtcacat tcaaacgatt ttgaagaagg cagtacaatt  1020

cgttatttgg ctgtaactct tcaagatatt ggcttttatc aaatcaaaaa aattgttgat  1080

tcaaaaaaac tgaatttaaa gatccatcag tcacacttgg ttgtacccta ctgtccaatt  1140

gcatctatta ctggaactgg aagcaatgat agatgtattg cgattcaga taatgtttct  1200

tttgaaattc aaggtgtgcc cccaatgaaa ttagcatact ctaagatcgt taatggtcaa  1260


24

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acttttttcat atgtagactc cagcttgcaa ccagaatatt ttgagtctcc tttgcagtca 1320

agcaaatcca aacaaagttt tactcaagga gaactaaacg atttgaaatg gggaagaaac 1380

caacctgtta atattaattt agactcttcc attacccagg acggcaaatt tgcatataaa 1440

attgataaaa taactgatgg tctgggaaat gtcgtggatt ttacatctct ccctgaagaa 1500

ttaaaaaagc gctatgatct atcttataat ttcaatgttc atgaggttcc acgtgcagcg 1560

ctagaagaaa gatttgatcc aaagtcaccc acaaaaaggt ctattgccat cgtgtttgaa 1620

gaaatcaaaa actggatttc agacattcca tatgttatta gcctatccta tactgatgca 1680

caagacaagt cgaaaaagat aatgaatgtt actacagatt ctttgaccaa agtgttgcaa 1740

gcggatcttc cggggtcata taacttagaa tatattgaat ctaagttttg tccaggtgaa 1800

attgtgggta aatcaaacgt tcttgtaact atgccagttg cacctactat ggaagttaaa 1860

tcatttccaa tattggacca gtgtgtggga caggttggtc taaactttga actatctttt 1920

actggggctc caccatacta ttataacact aaaatctata gcttgaaaa cggtgaaaga 1980

aagttatatg atgcaaagag atacacctct gaaggtacga gaaatcgctt cagctatagt 2040

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25

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<213>      Saccharomyces cerevisiae

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ttagctttcg acggggacgt aggaattaca tcacaagctc gagtaagaaa tcctcgagct  180

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27

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<211>      303
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      35

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ttaactcccc caagatttgt gaagatcatg aatagacgcc ctctgttcac agaaactagt      240

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taa                                                                     303


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<213>      Saccharomyces cerevisiae

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ccaaccactc tattgagcac gccagtacgt ctcaaaaatg ctttggaac accatcgccg      180

ccgtcaccac caggcataac gaaaagcatc actaaatcga agaaggcc gtcgacaacg      240


28

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      37

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ctacatttaa ttactgtgga gaatattaag cctgaagaaa tacttatatt ttcgttaaca 180

aacaaagcag ttgatagtat aatagaaaat ttactgtcca ttttcgaaaa ctcgcataca 240

aataaggaaa ttgtccatca gattgggtgt tacacagttc atgggttggc taatagaatc 300

gttgtagaga atgaggggat gataaacatt atagaagaga ttggatggag aggattaatg 360

aagttgttac cgccgtcaaa gagaaccccc catcatttca gatcatataa ggaactcgag 420

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29

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agcgttttca gacgtatata g                                          2121


&lt;210&gt;      38
&lt;211&gt;      3414
&lt;212&gt;      DNA
&lt;213&gt;      Saccharomyces cerevisiae


30

<400> 38

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gagaaaaatg tacctagatc aaacggaaga accaaaaacg aacacaatag tatggatgac   180

gaagagtttg aattcttcca tcaatttagt cgggagaaag ttaaaggcgt catacacgta   240

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ggtcaaccag tcaacgaaaa aaaacagctc agaattgttt ccaaggccga tgtctggact   420

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31

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32

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<213>        Saccharomyces cerevisiae

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<213>        Saccharomyces cerevisiae

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<213>      Saccharomyces cerevisiae

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44

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<212>      DNA
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<213>      Saccharomyces cerevisiae

<400>      45

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ggtataataa ccaaaatagc agcttcaccg ttcgtaattg ttctttattt caatactgca   180

ttttttaatc cttttaagac cctttacgaa aatgaaaaaa aaaagccaa gaaaaacttg   240

aaactgacgc gcgaaaacgc gtcactaagc ataaggaaaa tgcatcaata cagtgccatt   300

attccaagtg ggacctga                                                318


<210>      46
<211>      309
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      46

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cccagcatca ttgatgttac atatactatg cacgtttttt atatgacgat aatacttatt   180

ttggtcagga agcaaatgca gtccatacat gcgtttctgg gtagtttatg cttaccctcc   240

cacgtgctag attttttcgat tgtaagagat attttatcat ggtatttcct tgagacagtc   300

gcagtatga                                                          309


<210>      47
<211>      1110
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      47

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gttgatgatt taaaacctgg ttcctcgggc atagcagatc acaaatcttc caaaccacta   180

gaactgaata acacaaatat aaatcagctt gaccaatgga ttgagcattt gagtaaatgc   240

gagccactat cagaagacga tgtagcacga ctatgtaaaa tggcggtgga cgtgttgcag   300

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cttttcatgg gtgattacgt ggatagagga tattattctg ttgaaactgt atcttaccta    480

gttgccatga aagtcagata cccacataga attacgatac tgagaggcaa tcacgagtct    540

aggcagatta cccaagtata cgggtttat dgatgaatgtt tgagaaagta cggcagtgca    600

aacgtgtgga aaatgttcac agatctttc gattatttc ctataaccgc attagtagat    660

aataaaattt tctgtctgca tggaggactt tcccccatga tagaaaccat agatcaggtg    720

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caccaattgg taatggaagg ctatgcttgg tctcaccagc aaaatgttgt caccattttc    960

agtgctccta attactgcta cagatgtggt aatcaagcag ctatcatgga agtggacgag   1020

aatcataata gacaattctt acagtacgac ccatccgtaa gaccaggtga acctagcgtc   1080

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<210>      48
<211>      1557
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      48

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aaatggaaaa acatagttac aatcattgcg tccggttttg ctctgataag tgatggttac    180

gtaaatggtt caatgagtat gctaaacaag gttttttgtta tggagtacgg taagaaaaac    240

tatagctcaa aagtgtcgac tagagtttcc aacgcagccc tagttggtat tattttttggc    300

caattcttta tgggtatcgc tgctgattat tatagtagaa aatcttgtat ccttgtggcc    360

actgctatct tggttattgg tagtgctctg tgtgctgcct ctcacggtac tactgtacct    420

ggcatgtttt ggatgttaac agttatgaga ggtttggtag gtattggtgt tggtgcagaa    480

tatcctacca gtacattaag tgctaatgag tctgctaatg aatataccac taccaaaaga    540
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47

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ggtggtatcc tggttatggt gacaaatttg ccactagcct tcggtggtcc atttgctacg    600

atcatctttt taatcgtcta caaaatctgt tcaggaacaa aacatttaga ggcgatctgg    660

aggactgttt ttgcaatagg gtgcttctgg ccattgagtg tgttctattt tagatggaag    720

actgctacta cagaagtcta tgaaaaaggt agaatcaaga gaaatatacc atatttccta    780

gcattgaaat tttattggaa aaggttactt ggtacatgtg gtacatggtt tatgtatgat    840

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caaaatgatt tagtaaaagt ggcagagtgg aacttactgt tgggagtttt agctgtactg    960

ggtgtaccaa ttggtgctta tctgtccgat cgtattggtc gtaaatatac gttgatgttt   1020

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caacccatta gggataattt gggtgcaaga tggacttta ttattgctgc aatttgtggt   1320

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aagcaagacg ttgaatttca caactatttg gtatccaatg ctggactgg taagatggga   1440

tttgatgaga cagatgaaga atcaatggtt agaactattg aagttgaaga gaatggtact   1500

aattgtagta agaaaaacgc agaaataatt tcagtcagac aggtcgatca aagttga       1557


<210>       49
<211>       2706
<212>       DNA
<213>       Saccharomyces cerevisiae

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tacaagattt taaacaaat aggtgaagga agttttggaa aagtatattt agcgctccat    180

agaccaacac atcgtaaagt ctgcctaaag acgagtgata agaatgatcc caatatcgtt    240

agagaggtat tttaccatag acagttcgat tttccttata ttacaaagct ttatgaagtg    300

atagtgacag aatcaaaagt gtggatggca ttagaatatt gcccagggaa ggaattatat    360
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48

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gagaatattt tattagacaa aaatggaaat gcaaaattga cggattttgg ttttacgaga  540

gaatgtatga caaagacgac attagaaacg gtttgcggta ccacagttta tatggcacct  600

gaattgatag aaagaaggac ttatgatgga ttcaagattg atatatggtc attgggagtg  660

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aaatggaaaa tcgtcaatga agaaccgaaa tacgatgcta aagttattcc ggacgatgct  780

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gaaaattgca aatatccaaa aagaagcagg tccgttttat cagtcaaaaa agttattgaa  1140

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gaaataggct aaaagtagc tccagaacta ttattaaatg aacatatccg aatagaggaa  1740

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aattatgata gcgaatctgc ggaaaattct aggtctatat cttttgatgg aaaagtttcc  1860

ccgccaccga tacgaaatcg gccattgtca gagatatcgc aaatttctaa tgacacttat  1920

atatcagagt actccactga tggtaataat tcgtcattca aaatttcaga cactatcaag  1980
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49

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<211>    942
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<213>    Saccharomyces cerevisiae

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acctatcatt cagatgaatc tttaggcata aaacattcag attatataac ttcccaagat   180

gaaagaaat tgaggtcgga gatcatctcc gcagtgaaaa gagatctatc taaaaacaag   240

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gtgaaaaatt tgtccaccac attttgtgta attcaaacac tgtgtccacc agagactata   360

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attcaacgat acgaagagcc taactcaagc aaccgatggg actctccact ctttgctatt   480

cttactcctc aggacaacat aactgactac atcgacgata tttgtaaagt agtctttcaa   540

acttccaaat cggctaaaaa cagtggacac aatgatccgt tgagtaaggg cttacaaaaa   600

ccgaactcag ccacggtact aaagcctgcg tctcagtcca atttcatcca ggttctcgac    660

atcgaaacta gtaagataat aaaaaccata atgaaccaca tcaaaagcct gacttctatt    720

ggcgggggtaa gtaacggaac aagagtcatt gtttccgaag ggattaccga tatcaatgat    780

gatggttgct tcttcgtaga cttgcccatt ggtaacgtcg ttacgttggc gcaattgcag    840

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<210>      51
<211>      765
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      51

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tacattagct tagcttctga ttcttcctct ggattttcct taagcagtat gccagctggt    180

gttttggata tcggtatggc tttagcttcc gccactgacg actcctacac tactttgtac    240

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tcttctgctg ctccaacttc ttctgctgcc ccaagctcat ctgctgcccc aacttcttct    420

gctgcctcaa gctcttctga agctaagtct tcttctgctg ccccaagctc ttctgaagct    480

aagtcttctt ctgctgcccc aagctcttct gaagctaagt cttcttctgc tgccccaagc    540

tcttctgaag ctaagtcttc ttctgctgct ccaagctcca ctgaagctaa gataacttct    600

gctgctccaa gctccactgg tgccaagacc tctgccatct ctcaaattac cgatggtcaa    660

atccaagcta ccaaggctgt ttctgagcaa actgaaaacg gtgctgctaa ggcctttgtt    720

ggtatgggtg ctggtgttgt cgcagctgcc gctatgttgt tataa                    765


<210>      52
<211>      1407
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      52


51

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attcctgaag gttgtagatt aacgcaagtt caaatgattg gcagacatgg cgaaaggtat   240

cctaccagaa gtgaggccaa ggatattttt gaagtatggt ataaaatatc caattacaca   300

ggtaagtacg agggatcatt atcgtttttg aataatggat atgaattttt tattcccgat   360

gaaagtcttc tagaaatgga gacaactttg caaaattcga ttgatgtgtt gaacccgtat   420

acaggagaaa tgaatgcaaa gagacatgca agggagtttt tagcaaaata tggaaaattg   480

atggagaact gtaccaactt tcctatcttc accacaaatt cgaaaagaat ctacgatact   540

gcgcaatatt ttgccgaggc tttgggcgat ggctttaata tatcacttca aacacttagc   600

gaaaattcct cgtcaggagc aaacacatta gctgccaaaa gttcgtgccc caattggaat   660

tcgaatgcca acaatgatat attaatgtca tattcgaggg actacttaga aaatatttcc   720

gatcgtctta atgacgaaaa taaagggctg aacttgagca ggaaagatgc agcggccttg   780

ttttcttggt gtgccttcga gttgaacgca aaaggttata gtaacatttg tgacattttc   840

tccgcggcag agttaataca ttattcttat gagactgatt tgacgagctt ctaccaaaat   900

ggtcccggat acaaattgat taaatctata ggtgctaatt tgttcaatgc aacagtgaag   960

ctaatacgac aaagtgcgca cttggaccaa aaagtttggc tgagctttac gcacgatact  1020

gatattctaa attatttgac aactgctgga ttgattgatg acactagaaa tttaacaacc  1080

aatcatgttc cctttcgtga tcattcctac cacaggtcgt ggtacattcc tcagggagct  1140

agagtctaca cagaaaagtt tcaatgctca aacgattcgt acgtccgtta tgtggtcaac  1200

gatgctgtgg ttcctataga gagttgctcc agtggtccag gtttttcatg tgaagagggc  1260

acattttacg agtatgccaa agacagatta cgaggtgtga gcttctatga agattgcgac  1320

gtctccaaag ttagcaaaga aaaggaattg acgttttact gggattggaa cacaacaagg  1380

tataacgcat ccttagtgaa tcaataa                                      1407
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<210>       53
<211>       1863
<212>       DNA
<213>       Saccharomyces cerevisiae


52

<400> 53

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gactcattaa aacatatagt tgacgccaga aacagcttat cagagacact gctaaatagc   180

aacgatgatg ggagtataca caattctgac cagaatactg gtttgaataa agacaaagag   240

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gagctcaaac aatttcttcc catttcctta gaccaacaga ttcatacagt atctttacaa   360

ggtgtctctt catcattttc tcgcggacag atagaatcat tgctagacca ctgtttgaat   420

ttagcgttga ctgaaactca aagcaattcc gcattgaaag tagaagcttg gtcttctttt   480

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aacattgaag atcaaacaga cgaaagaaat tcaaagaaag aacagttgga tgactcttcc   780

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ttgtgcaagg atataataga atttaggaca aaagttgtca gtatagagaa agaaaaaaaa   900

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caaataagga aaaccactc aggagccaaa gggagcgcca atacagagga ggaggatact  1020

aatatggaag atgaagatga ggaggatgac actgaagacg accttgcctt agagaagaga  1080

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aaggccatat ctgcagggaa ggctgccgcc atcacccttc ctgaaggcac tgtgaagagc  1440

gagaactata cgcggacaa gaatgtgtct gagagctcag aacacgtcaa gatcaaattc  1500

gactttaaga aggctattga tcactcagtt gaaagctcta gcgaagacga gggatacaga  1560

53

gagagcgagc tacctccaac aaaaccctcc gagagaagcg cggcagagga ccgtttgcca 1620

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gaactggtgc gtgaattcct cggcgtctac gaggacgagc tggtggaata cattcttgag 1740

aacatccgcg tgaaccagag caaacaggcc cttttaaatg agctaaggga gactttcgac 1800

gaggacgggg aaacgatagc tgatagactg tggagtcgta agaatttcg cttggggacc 1860

tga                                                              1863


<210>        54
<211>        474
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        54

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aaatgtctcc tatcatgcag cgcaggctgt cctcctttt ctttctccct ttccttttgt    180

aacaacgatc ccaagtttac ttcagtgctt ggtcttggga ccaccggatt atcattcact   240

gctatgacag gtaatctaga agatgatttc gaaaagtgtg caacatttgt tttagcttgt   300

agaggttccg gctgcggctg cggctgtaga ccggattctt ttatcttcac tgcgtcgcca   360

ctggaagccc ttcttccctt acaaaagcct cttgggaatg aaggaggtaa cagggtacag   420

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<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        55

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tacgtttctg atattggcgc ccatttatct gaatattacg ctttccaggc tttgcataag   180

actgaaacat acccacctga aattgccaag gctgttttg ccggtggcga tttcaccacc   240

atgttgactg gtatttcagg tgatgaagtg accagaatga tcaccggtgt gccatggtac   300


54

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caagctactg tttcatctga atctagctct gctgcaagca ccattgcaag ttctgctgaa 540

agttctgttg caagctctgt tgcaagctct gttgcaagct ctgctagttt tgccaatacc 600

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gacagcaccg tcacaaagac tcaagcttcc actgttgaaa ctaccataac tagttgttca 720

aataacgtct gttcaactgt gactaagcca gtctcctcca aagctcaatc tacagctact 780

tctgtcacat cgtcagcatc tcgtgttatt gacgttacca ctaacggtgc taacaagttc 840

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<210>    56
<211>    2508
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    56

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aaaaccgcca ccgccatttt aagaagaaag aagaaggaca acatgctttt ggtggacgat    120

gctatcaatg atgacaattc tgtcattgct attaattcta acaccatgga caaattggaa    180

ttgttccgtg gtgacaccgt tctcgttaag ggcaagaaga gaaaagatac tgtcttaatt    240

gtgttgatcg atgacgaatt agaagacgga gcatgcagga taaaccgtgt agttcgtaac    300

aatttacgta ttaggctggg tgatttagtt acaattcatc cttgccccga tatcaaatac    360

gctactagaa tttctgtgtt accaattgct gatacgatcg aaggtataac tggtaatctt    420

ttcgatgttt ttttgaagcc ttattttgtg gaagcctaca gaccagtgag gaaaggcgac    480

cattttgttg tcagaggcgg tatgagacaa gtcgaattca aggttgtgga tgtcgaacct    540

gaagaatatg ccgtcgttgc tcaggatact attattcact gggaaggtga gccaatcaac    600

agggaagatg aagaaaataa tatgaatgag gtgggttacg atgatattgg tggttgtcgt    660

aagcaaatgg ctcaaattag ggaaatggtt gaactaccat tgagacatcc tcagttgttc    720

aaggctatcg gtatcaagcc accaagaggt gttttgatgt atggtccccc tggtactggt    780

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gaagaagccg aaaagaacgc tccagccatc attttatcg atgaaatcga ttctatagct    960

ccaaagagag acaagactaa tggtgaagtt gagagaagag ttgtctctca attgttaact   1020

ttaatggatg gtatgaaggc aagatctaat gttgttgtca ttgctgctac caatagacca   1080

aattcgattg atcccgcttt aagaagattt ggtagattcg atcgtgaagt cgacattggt   1140

atcccagatg ctacaggtag acttgaagtt ctacgtattc acaccaagaa catgaagttg   1200

gctgatgatg ttgatttgga agcattggct gctgaaacac acggttacgt gggtgctgat   1260

attgcctctt tgtgttctga agctgccatg caacagatcc gtgaaaaaat ggacttgata   1320

gatttagatg aagatgaaat tgatgcagag gtgctcgatt ctttaggagt caccatggac   1380

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agtgtcaatg ttacttggga tgacgttggt ggcctagatg aaatcaagga ggaattgaag   1500

gaaactgtag aatacccagt cttacatcca gaccaataca caaagtttgg gttatcacca   1560

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ggtgatgctg gtggtgcttc ggatagagtc gtcaaccaac tattaacaga aatggatggt   1860

atgaatgcta agaaaaatgt gttcgtgatt ggtgccacca taggccaga tcaaattgat   1920

cctgctattt taagacctgg cagattggat caattaattt atgttccatt gccagatgaa   1980

aacgctagat tatctattct aaatgctcaa ttaaggaaaa caccactaga accagggcta   2040

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gtgcagaggg ctgctaaata cgctatcaag gattctatcg aagctcacag acaacacgaa   2160

gctgaaaagg aagtgaaagt agaaggtgaa gacgtggaaa tgacagatga gggagcaaag   2220

gctgaacaag aaccagaagt agatcctgtt ccatatatta caaaggagca tttcgcagaa   2280

gctatgaaga ccgctaaacg ttctgtttca gatgctgaat gcgtcgtta tgaagcatac   2340

tcacagcaaa tgaaagcatc tagaggtcaa ttcagtaatt tcaactttaa tgacgctcca   2400
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56

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gctgcatttg gttctaatgc ggaggaagat gatgatttgt atagttag        2508


<210>      57
<211>      651
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      57

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tgcccacgta aacccattga gataaagtac ttttcacaga tatgtaacga tatgatgaac   120

aaaaaggacc gattgggtga tattttgcat attatcttgc gagcatgtgc actcaatttc   180

ggggcgggtc cccgtggtgg cgctggtgac gaagaggatc gatctattac gaatgaagaa   240

cccattattc cctctgtgga cgagcatggc ctgaaagtat gtaagttgcg cagtcctaac   300

actccacgaa gactcagaaa aacactagat gccgtgaaag ctttattggt gtcgtcttgt   360

gcttgtaccg caagggattt agatatattt gatgacaaca acggcgttgc aatgtggaaa   420

tggatcaaaa ttctgtacca cgaagtagcg caggaaacca cgctgaagga ctcttataga   480

ataactttgg taccttcttc tgatggtata tcagataccc ttaccgttat ccagagcttc   540

agctactcgc ttttgccggt cctcagcgca acgtatacgt cgatgataca acaagacgca   600

tccaactgta cactgattac aacaagaacg gttcatcgga gcctcgacta a              651


<210>      58
<211>      345
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      58

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agaagtggcg cgctcttaat taaaatgatg cagcgtgtta tcacatcttg cgttaccggg   120

ccttgcaaaa attgctatgt ttttcttgtg cttggtattg cttcgtggag atatatattc   180

tcatatcagg acggaatttt acaaagtgag aactctaaat ggtgtagtaa agagaagaaa   240

aaaaaatgct cagcgattta ccctcattac aaccaccgag attcactagg aaacggagct   300

gtccctcgga atttattgtc aacatatcat ccaatgttaa tgtag                    345


57

<210> 59
<211> 552
<212> DNA
<213> Saccharomyces cerevisiae

<400> 59

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gccccgaaat tgagtgcaca tgctcgcaag ataatatgca aaatatcacc caatcggtcc   120

ttttttgttca tcatatcgtt acatatctgt gaaaagtact ttatctcaat gggtttacgt   180

gggcatagat cacgcttcag ccgctctgtg tcgactttct tttcgccagg taaacttgct   240

tgcatagctc atctacgtgt aggctgccaa attgtaccca tatttcctta tggtgctttt   300

ctgaagactc cttacaatag gtgcgccgga aacaaagtca gtgaaagtac gcatcgtaga   360

gctgtcgttc ggcctagcac tcgctatttc gtgacaacgt tccaggacac ggaaactcaa   420

ctcattatag tatcctctgt tgaggtaaaa aagagaaagg gtatcgtaat cctttctatt   480

gaatttcaaa gtatgcactt gaaacaacgt gtagaccatc aagttgattt tcttgggaac   540

aagatacttt ga                                                        552
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<210> 60
<211> 1599
<212> DNA
<213> Saccharomyces cerevisiae

<400> 60

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atctcattgc aaagaccgtt gggtctagat aaggacgttt tgctgcaagc tgcggaaaaa   120

tttggtttgg acctcgacct ggatcatctc ttgaaggagt tggactccaa tgtattggac   180

gcttgggccc aaatagagca tttgtaccca aaccaggtta tgagccttga aacttccact   240

aagccaaaat tccctgaagc aatcaaaacg aagaaagact gggactttgt ggtcaagaat   300

gacgcaattg aaaactatca gcttcgtgtc aacaagatta aggaccctaa aatcctgggc   360

attgacccaa atgtcacaca gtacacgggt tacttggatg tggaagacga ggacaagcat   420

ttcttctttt ggacttttga aagtagaaac gatcctgcaa aggatccggt catcctttgg   480

ttgaacgggg gtccaggttg ttcttcacta accgggctgt ctttgaatt aggaccctca   540
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58

tccattggac ctgatttgaa acccatcggg aacccttact cttggaacag caatgccacc   600

gtgatcttcc ttgaccagcc tgtcaacgtt gggttctcgt attccgggtc ctcaggtgtt   660

tccaacactg tcgccgctgg taaggatgtc tataacttct tggagttgtt cttcgatcag   720

ttccctgaat acgtcaacaa gggccaagat ttccacatcg ctggggaatc ctacgccggc   780

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cgtaccggca gaaacgttta cgatatcagg aaggattgtg aaggtggcaa tttgtgctac   1140

ccaacgttac aagatatcga cgactactta aaccaggact acgtcaaaga agctgtcggt   1200

gcggaggttg accactacga atcctgtaac ttcgatatca acagaaattt cctgtttgcg   1260

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actgcttcta tcaccgacga ggtcgctggt gaagtcaaat cctacaagca cttcacctat   1500

ttgagagtct tcaatggtgg ccacatggtt ccatttgacg tccctgaaaa cgccttaagt   1560

atggttaacg aatggatcca cggtggtttc tccttataa                          1599

<210>        61
<211>        1107
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        61

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ccacataacg ccaaattcga agtatcgata ttaaacaaac tgggcaacaa atgtaagcac   180

atcttacctc ttctagagtc taaggctacc gataataatg acctattgtt gttgtttccc   240

tttgaagaga tgaacctta tgagttcatg caaatgcact ataaaagaga tagaagaaaa   300

aaaaatccct attacgattt gctaaatccc agtatcccaa ttgttgcgga ccccccgtt 360

cagaaatata ctaatcaatt ggacgtcaat cggtattctt tgtccttttt ccggcaaatg 420

gttgaaggga ttgcattctt acatgagaac aagatcattc accgcgacat caaaccgcaa 480

aatatcatgc taacaaacaa taccagcacc gtatccccaa agttgtacat aattgatttt 540

ggcatctctt atgacatggc aaataactca caaacaagtg cggaacccat ggatagcaag 600

gtgacggata taagcacagg aatttacaag gccccagaag tgcttttttgg agtaaaatgc 660

tatgatggtg gcgtggacgt gtggtcgttg ttgataatta tttctcagtg gttccagaga 720

gaaacaagcc gtatggggca cgttccggcc atgattgatg acggcagcga cgacatgaac 780

tcagatggaa gcgatttcag actgatttgc tcaatattcg aaaagttggg cataccgtcc 840

attcagaaat gggaagaggt tgcgcaacac ggctcggttg atgcatttgt tggtatgttt 900

ggtgcagatg gcgatggcaa gtatgtactg gaccaggaga aagatgtaca gattagcatt 960

gttgagagga atatgcctcg actggacgag attgcggatg tcaaagtcaa gcagaagttc 1020

attaattgta tcctggggat ggtttcattt tcaccaaacg aaagatggag ctgtcaaaga 1080

atcttgcaag aattagaaaa gccataa                                      1107


<210>      62
<211>      1647
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      62

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tcggacctat acaacaaaga acgagatgga agtacggaag agactttaaa ctctttgaag  180

tttttacata aacctcagag agtaactcaa atgagagcga acaggttccc agaggaagaa  240

gtgcaaagaa acactgattt aaacaaaaga attttctccg cagggaatga tgaaaacgtt  300

gataatgaga gcggctggtc aaaaattgcc gctgccaaga tcacacttc cgtagaatca  360

ttaaatggca gtacgagacc cccattcaaa atagagctgc ctcccctttc ccccaaatcc  420

accgtaccaa aatctttttca agcagaatat cccgaagcta agtcacctgg caatgatatg  480

aattttgaat atgatgaaga aattctaatt ccatttgcgc cacctgtata taaaaagtca  540

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ggtgaactat tgaagagctc attgaagaga agatcaaaat cattacctac aaccccaggt   600

ataaggagcg ggaatggtgt ccaagcaaga gacggtagtc cgatgttgat taggagtaag   660

agtgttcact ttgatcaggc ggcacctgta aaatattttg ctgaggatga aagccctata   720

aacgttaata aaactgaaca acacgataat tgtctaagct ttaagcataa gccagtgaat   780

ttaatggtgg acccggaaga agagacaaaa atgctatcat ctggattaga aacgacatcc   840

atagatgatg acttgacgac agttgcgcca aaaggcttcg cacatcctgc taaaatttcg   900

aatccaaaca atggtaaagg caccaacaat acaaaattaa gaaaaagtaa aagatttcag   960

aacctcctaa agaacaggac cgacatgcca ccatcaaaat caaataaaaa attcgttaat  1020

ggtggcggtg ctcatgaaat ttcagatcgt aattcaaaaa attaccatgt tgttggatta  1080

tacagcaaga acttccccat tttaagcaac aagaatccta aaagtttaaa gctgaacatt  1140

tttatcaatt tatcacaaaa taagaaagtt tttctacaag aattgtcatt atacatccat  1200

agagacaaca attactttc aaattcctcc tcattttata atattcccaa tagccacaat  1260

ggtaatgact gtaatggtgt ggccaagggt tataacgctg gctgtacaag attaattgct  1320

ggaaggatac tagtgaaaaa cattttctat gataaaagag tggtggtacg atatacgtgg  1380

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<210>      63
<211>      1593
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      63

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gtagaattgc atagaaccaa cgaattcatt gataataagc cgtccttttt caataggatt   180

gcagctgctt taaatgctga gacgaaaggt attgaaccag ttacagaaga tgaaaaaaat   240
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gatgactcga tactcaatgc cgccactata tggttttcag ctaatatggt gattgtagcc    300

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gttatcattt ttttcaatat tttgggtttg atccctgttg cattattctc actttttggg    420

gtagaactgg gcctaagaca gatgattcta tcgagatatt tggctggtaa catcacagca    480

agattttct ctcttgttaa tgtcattgct tgtgtcggtt ggtgtgtttt aaatatttct    540

gtttctgctc aactttttgaa tatggtgaat gaaggctctg ggcacaactg tcctatttgg    600

gcaggttgtt tgattattgc tggtggtacc gtgcttgtga ctttttttgg ttacagtgtc    660

gttcatgcat acgaaaaatg gtcgtgggta cccaattttg ctgcctttt ggtcattatt    720

gcccaactat cgagatcagg aaaatttaaa ggtggtgaat gggtaggggg tgcaactact    780

gcaggtggtg ttctttcttt tggttcatct gtttttgggt cagctgcggg ttgggcgact    840

tatgcagcag attacactgt ttatatgcca aagaccacaa gtaaatacaa aattttttt    900

tccgtagtag ccggtctagc gttccctcta tttttcacca tgattcttgg tgctgcttgc    960

ggtatggcgg cccttaatga cccaacctgg aagtcatatt atgataaaaa cgccatgggt   1020

ggtgtcatat atgctatcct ggtccctaac tctctaaacg gattcggtca attctgctgt   1080

gttttgttgg ctctttcaac tgttgctaat aatgtccctg gaatgtacac tgtcgcttta   1140

tccgctcaag ctttgtgggc acctttggct aaaataccaa gagtagtctg gacaatggca   1200

ggtaatgctg ccactttagg tatttccatc cctgctacct attactttga cggctttatg   1260

gagaatttta tggattccat tggttattat ttggctattt atattgccat tgcatgttca   1320

gagcatttta tttataggcg ttccttcagt gcttacaata ttgatgattg ggataattgg   1380

gagcatctac ctatcggtat cgcaggtact gctgcctaa ttgctggtgc ctttggagta   1440

gcgttgggta tgtgccaaac ttattgggtt ggtgagatca gtcgtttgat cggagagtac   1500

ggcggtgaca ttgggttcga gttaggcgga agttgggcgt tcatcatcta taacattgta   1560

agacctttag aactcaaata tttcggtcga tga                                1593
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&lt;210&gt;       64  
&lt;211&gt;       651  
&lt;212&gt;       DNA  
&lt;213&gt;       Saccharomyces cerevisiae  

&lt;400&gt;       64  

62

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aaaaaggacc gattgggtga tattttgcat attatcttgc gagcatgtgc actcaatttc     180

ggggcgggtc cccgtggtgg cgctggtgac gaagaggatc gatctattac gaatgaagaa     240

cccattattc cctctgtgga cgagcatggc ctgaaagtat gtaagttgcg cagtcctaac     300

actccacgaa gactcagaaa aacactagat gccgtgaaag ctttattggt gtcgtcttgt     360

gcttgtaccg caagggattt agatatattt gatgacaaca acggcgttgc aatgtggaaa     420

tggatcaaaa ttctgtacca cgaagtagcg caggaaacca cgctgaagga ctcttataga     480

ataactttgg taccttcttc tgatggtata tcagtatgtg gaaactttg gggagagttg      540

aacaactgct tccatatgcc agcctcattt tgcgtaatcg agaagttttg ttcagagaac     600

cgaagcgagg aattgacgag tatctggaaa acgattcttt tcttcaaatg a              651


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<213>       Saccharomyces cerevisiae

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aagcgacaat gtgttgagga aaattacgat aaaaaatttt ctatgattaa aaaaaaacgt     180

cagcaaacat tacaaaagta caagcttagt cttctgaatc cgttggaaag ggcttttcgc     240

cctttatcat atgaaaagta catgattggt ttaaatatgc agtatgcatc gcattctctc     300

actgaaggtc atcactcaca tagttctgct aacgtaaaat cactcaattt tccacacagg     360

atacagatag gagtattagc aaattgtatt ttattggtaa ctcaagaagg atgttttcat     420

agtaaattag tatttgcaac aaacaagggc tatgtcgcag attttcatc cctggataat      480

ttttctgaag aaaatttctt tacggggttt tccatggctg aattaaatcc tatgttgaaa     540

tataagtccg agccaactga tgtgttcaaa acaatgaaac ttgagagaac agttgccatc     600

aaggaagggc cgagccatta tttttatcac aacgttaata ccagatctaa cgtgcatact     660

tttgccatct ttttacaaga cttttcttcc ttaaaactgc tcaaaattcg tcaggtcaaa     720
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63

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ctcaaagaaa attgccaagt ccatgattct cttgttgttg gagacacgtt gattattacc    780

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ttacagtact ccaagaccaa cggtatgaca tcagaaagtc gaaatcaacc tatcagaaat   1080

tccctaaaat ctgttgtttc cataaaagca ttgaataata aaggcctaat acttatatct   1140

ggaatggcag acaaagagaa tgtgcaacaa ctggttatag cagatacgtt cctggaggac   1200

attctgaccg aaatcccggt tgtatctttt aaaactaagt cttaaacgt gactaaggat    1260

acagaaatac tcgagatatc ggatgacggg cgctacttca tttatggttc aactagcgct   1320

agggacggaa agggtgattt tgaagtattt tgtaccactt tatctggaaa tcttgactac   1380

gaaaaatccg aaggtggaaa tatcaccctc tatccaatag gaggtatgaa gaactactgt   1440

aggttagaaa acttccagtt tgaatctatc cacctacatt cggctttcat acccccaagg   1500

tacgtaaatc cgtttgatgc tgtggaacct ctaggtgaag agagcagtac ttcaccttac   1560

gatatacctg aagaagcact ttctcaaaaa atatgcatct taattcggag agaagatgat   1620

ccctacaatg gggccaatat cttcataaca tctgctttga cctag              1665


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<211>      405
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      66

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acacatatat tggtaagctt ccaggaagac aattgggtat ttggattatc ggccgtattg    180

agaatccttt tctttataca acgcatagaa tctttgggat ttacccttct agatcttaac    240

acatctgaaa tttccaacgc tatggggaga tcaaggtcac cgttgggaat gctctcacta    300

gtggcttgtt ctattaatgc gtctaactca cttggcgtgc taacggacat actgttctta    360

gttctttact cactactcat tcaccttagc aaaaaaaaat cttga                    405
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64

<210>     67
<211>     336
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     67

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tcccataacg gtgagtgtgg caacgccagc agtgaaatca ccacagtttg gataatagaa     120

catatgaaaa acaacctcgt aactaaatgg ttgaatcggg tcttgcacac gtcgctaaag     180

atggtatggt acgtgtaccg tggattcaac aactcccttg gcgtctgtat catctgcttg     240

ccctgtaatg tcctttcgtc ttctcaatca cacttactca tcgccaaaga gtctgctctt     300

cccgttagtg attctcgatg ttattatatt ctttag                              336


<210>     68
<211>     366
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     68

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gtggtttggt ttatgccagg tgaatccttg ctacttaatg gaaatgcaga atcggttttg     120

gaagttagtt cggtaacaaa tgtagtagat tctttttcat tctcgaaggc tggagaagta     180

gccggcttga atccgtcaac tacatctgcc caatattcct tttcaatgg gtttctaggc     240

attttttgatt ttgaggttgt atatctgtat ttgtgtacta atgagtcaga tagcgataat     300

attatacgtc aaaaaaactt gggaaggaca atgaattgta ataacgctga tgatatgttg     360

ttttga                                                                366


<210>     69
<211>     597
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     69

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gatgactctg caattctatc agtcggtggt aacgttgcgt tcgaatgttg tgcacaagaa     120

caacctccaa ttacatcgac ggattttaca atcaatggta ttaagccatg gcaaggaagt    180

ttgcctgata acatcggagg gactgtctac atgtatgcag gctactatta tccgctgaag    240

gttgtttact ccaatgccgt ttcctggggc acgcttccaa ttagcgtgga attgcctgat    300

ggtactactg ttagtgatga cttgaaggg tacgtttact cttttgacga tgatttaagt    360

cagtcaaatt gtactatccc tgatccttca aaacatacta ctagcatcgt cacaactact    420

accgaactgt ggactggtac ttttacttct acatctactg aaatgaccac cgtcaccggt    480

actaatggtc aaccaactga cgaaaccgtt attgttgcca agctccaac cactgccacc    540

tcatccagtt tgtcatcatc ttcttcagaa caaatcacca gctctatcac gtcttag      597


<210>        70
<211>        1554
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        70

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gaccaaagaa atggaactat tttttcgagt acatattcaa aatctttaag tagagaaaat    120

gacgctgact ggcattctga tgaagtcacg ctcggaacaa attcttccaa agatgattct    180

cgtctgactc tgcccctaat agcaacaact ttgaagagat tgattaaatc gcaaccggca    240

ttgtttgcaa ctgtaaacga agaatgggaa ttcgagccat tgaagcagct gaaaacttcc    300

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cacgacgtat tgtttgatat attttcagca gctaactttc acaaattatt tttaaaagag    540

ttaaacgaaa tcagcacagt aacacactct gaagatagga ttttgtttga tgtcaatgac    600

atcaatctct cagaattaaa atttcccaaa tcgatatatg atagcgcaaa attacacctg    660

cccgctatga caccacaaat cttccacaag caaactcagt cattttcaa atcaatatac    720

tataacactt taaaaagacc tttcggctat ttaaccaatc aaacttccct cagctcgtca    780

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gggacaacag tatttgggat agtaaacaac caaaggttta actatttaaa gtcaatcgtt    900


66

aatcaagagc atatatgtct aagaagtttc atctgtggta ttgcaatgat atgtttaaaa    960

cctctcgtta aggatttcag cggtacaata gtatttacta ttcccataaa tttaagaaac   1020

cacttaggct taggtgggtc attgggtctc ttcttcaaag aactaagggt cgaatgtcca   1080

ctttctctaa ttgatgacga actttccgcc aacgaatttt tgaccaacag taacgataac   1140

gaggataatg atgatgagtt taatgaaaga ttgatggaat atcaatttaa taaagttaca   1200

aagcacgtta gcggtttat tatggcaaaa ctgaggagtt gggaaaagaa tgggtttaat    1260

gatgacgata taaggaggat gaagtatgac aatgacgacg atttccatat ccaaaattca   1320

aggacaaaat tgattcaaat caatgatgtt tccgacatat cgttatcgat gaacggcgat   1380

gacaaatctt tcaaaattgt aagtacggga tttacaagtt cgataaatcg ccccacatta   1440

atgtctcttt cctatacata ctgtgaagag atgggcctga atatctgtat tcactaccct   1500

gattcgtata atttagaatc ttttgtagaa tgcttcgaat cctttattga atag          1554


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<211>      315
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      71

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tctgtgggtt gtgccttggt ggaagccaat cttctggtgg aagccaaagc agcagcggca    180

ggtcttgcgg ccttggtaga gttaattaga gttctcgata gagaacgaat agcagcagta    240

cgagccaaca ttattatatg tgcgtgtttt ttttatttat tttgttactg ttcttgcgat    300

agttatgaga gctga                                                      315


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<212>      DNA
<213>      Saccharomyces cerevisiae

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67

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cgccttaagc atagtgataa cgatataaac tggcgctctc tcgtttcaat actcaattct    180

gaagcctggg aaaacgaaaa gtacagagac atactaaatg gaagaaagtg gaggaccctg    240

gagttcgaga atgaccacca ctctgtgggt aatatgcata ttggaacagc gtgtacgcgt    300

ttatgcttcc cctctgagac aatttattac tgttttacgt gctccacaaa tccattgtat    360

gaaatatgtg agctttgttt cgataaagaa aaacatgtaa atcattctta tgttgctaaa    420

gtggtaatgc gcccagaagg cagaatatgc cattgtggtg accccttgc ctttaatgac    480

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agtaacgtaa ccgatgatga aaacgtaatc tccctattga attatgttct ggattttta    600

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tcctccctaa tgcatcctaa tcaaaacagc attactgatg atataatgga aaaacacgaa    720

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agaaaagaag cacatatgga gtgggctatt caaatcgaag aagaagagtg taacgtacac    840

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caagacccca gcatagcaaa tatgactata agctcgggat tcattgaacg aactattaga   1680

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68

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69

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ggtgataata ataataaccg cagcaataat ttcatggacg tcaaacagcg tgaaatagag 4980
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70

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<211>       2505
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       73

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gagtccagtt ccggtgaaag taaaagtaaa agcaaactaa atcttgaata ttctgcagat  180

atcgagccat tgaagttcag aatgacaaaa actaataata caaatgacaa attaaaatat  240

agtaacaacg gcaacgccac tgattcattt atgagactaa aggaacattt acagagaggc  300

aatactttaa attcgaatct tagggtcaat gagtttacc ctttcaattc cattg ataca  360

gagcaatttg aaaactattt gagagagcca aaatacatta aaatgttgaa acgtcggaaa  420

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aaagttattg gctctccagt tgaaagagcc gaattggact cgagtgcgga atcaaataaa  660

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cacaaatgca ggttatggtc tatactggat gatgaagtta gctttgagta cgattgtcaa 1080

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aagggattgg ctcggtccgg aagtttgaga agcatattta gtaaatcaat gagtaggtct 1620

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aaaacactcg gcagtaatgc acagccaaga acaccaaggg aaagcatgtc atctattttc 2340
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72

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<210>      74
<211>      1608
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      74

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tcgaatttta ctgtttacgc ggaattgaat aaaggtgtta ataagagaca actaatgctt 180

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gagttcatcg aagatcaagt catcattgac tatgatcgag actacactga aatttctaaa 720

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atgaacatgg acatgagcgt ggttcagggc actctacggg atcgtggcga atgggaatcg 1560

ttctgcaagc tcttctacca aaccatcggc gaatttgcgt cgctttaa              1608


<210>      75
<211>      939
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      75

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gaggacttca acgagcaaaa cgacgagctg aacagtcaag agaaccacaa cagcagtgag   180

aatgggaacg agaatgaaaa tgaacaagac agtctcgcgt tggacgacct agaccgcgcc   240

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agtgcggttc ccgtaaccat ttcgccgaac ttggtcgcta ctgctacttc caccacatcc   420

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ccgaaaccga aaccgaaacc aaagcaatat ccgaaagtta ttctgccgtc gaacagcaca   600

agacgcgtat caccggtcac ggccaagacc agcagcagcg cagaaggcgt ggtcgtagca   660

agtgagtctc ctgtaatcgc gccgcacgga tcgagccatt cgcggtcgct gagtaagcga   720

cggtcatcgg gcgcgctcgt ggacgatgac aagcgcgaat cacacaagca tgcagagcaa   780

gcacggcgta atcgattagc ggtcgcgctg cacgaactgg cgtctttaat ccccgcggag   840

tggaaacagc aaaatgtgtc ggccgcgccg tccaaagcga ccaccgtgga ggcggcctgc   900

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74

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<211>    588
<212>    DNA
<213>    Saccharomyces cerevisiae

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ccattgattt ggcagctgct gcaatcctct atcataaata agttgattca cattcaatcg      180

aaggagaact acccttggga gctgtataca gatttcaatg aaattgtgca gtatttgagc      240

ggcgctcacg gaaacagcga cccagtatgt ctatttgtgt gcaataagga ccctgatgta      300

ccgcttgtgc tcttgcagca aatcccgcta ttatgctata tggcgcccat gacggttaaa      360

ctggtgcagt tgcccaagag tgccatggat accttcaagt cggtttctaa atatggaatg      420

ctgctgctgc ggtgcgacga tagggtcgac aagaaattcg tatcgcagat ccagaagaac      480

gttgatctgc ttcagtttcc ctggttaaat gctatcaagt atcggcccac atctgtcaag      540

ctgttgaaaa ctacagtgcc aattgtctcg aagaagaggc aaaagtag              588


<210>    77
<211>    2352
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    77

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gtatatgtgg aagagatggg gatggaagaa ccgcaggctc cggaagcctt tagtgagaaa      180

gtccagcgat ttcgtatgtg ttttgaaaat aacgtggtga ttccagtaaa gaaaaatgta      240

gtggatccgc tagcacaaat gatttccctg cctctgaga aattcgattt gttcttaagt      300

aaaataggta atgttatggt aatgaggaga atattttaca tcatgatgat gtctatcatt      360

gcagcgttga ttattgcgag tgataggtta ccgaatggaa aagctcgagg ttcaaatgga      420

tcattctcgg accatgatct ccttttacag tatgctcgga atcgataga cctttcaaag      480

atagaaagag atttagagta tattagtagt atgccccaca tgtcaggaac aagtggtgat      540

gccgctatta gacattatat taaagagtcg ttcgacaaaa atggtataag gctagctggg    600

gaagaggagt tcatggcgta ttcgaattac ccaggaaatg tctcacttcg tgtatattca    660

aaggatgata cagaagggtt tgatattccc ttaaatgagg agaactttaa cccaatgagc    720

cataatggtc aattgaacaa cataccggtg atttatgcta ataaagcatc gttggacgat    780

atggcttcta tgcaagatca agggctttta aacggtgact ttattttact agtgcattac    840

ggagattatg ttttccaaca aatgttgact gctcaagaat atggtgcgaa agcaattatc    900

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ccgcagtatg gtactggtga tgcacttacg cctgaatggg aaggatcaat aagagatcct   1020

atcgatgcta cggaagccaa gtgcctaccc aaaattccat ccataccgat atctgccaat   1080

caaggagata aaatactagc tatattatca gacactggcg taaagttttc taataattta   1140

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gccacggagc tgatggaaaa gagaacagag gcattgaaga gtgaaatata caccattatc   1500

gacgtcggcc aaatcggtat atgggatgat agtaacaatt tagagataca atgtcatccg   1560

ctactagtag atcttttca aaaaaacatg acaagccgta aatttaacgt taaagtggat   1620

aatgttcacc agttcggcga ctggacgccg tatctagcgc aagggattcc agttgcgatc   1680

atttcatctc caggagtcat gaatagagaa catccgatct acacagtaga agacaaattc   1740

gatttcatca agataaact aagagacaaa aagaagggag aggtactttc tgagataatg   1800

ctatatcttg tcgaaaaatc actcgagctc attgacgatc cattcatccc attcagcata   1860

tcgaactacg tagatttcct ttcaactacg ttaaaagacc tccaaaaaga atgtcctgat   1920

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ttcgaaaaat ggaaaagcga atggacagag cttatgtatg gagccggtac atatatagaa   2040

cccactatca ttgccattaa tcgttggtca tggaactacc tactttccct aataggcgtt   2100

acccaatgtt tggaggaagg gttaatggat agaacctttt acaagaacgt tatcttcggg   2160

76

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gacactattg caatcaagga ctggagctct gtgcaggttc aagctaacac actcggcaca 2280

attttacaaa atacagcacg ctattttctt gagaataaaa accttcatgg aataaacacg 2340

aacgaatttt ag                                                   2352


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<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    78

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aagtctatgt catatttgaa aatatttgct actttaatct gtattctttt ggtttgggac  180

caagttgcat atcaaatcaa gaaaggttcc atcgcaggtc caaagtttaa gttctggccc  240

atcatcggtc cattttggga atccttagat ccaaagtttg aagaatataa ggctaagtgg  300

gcatccggtc cactttcatg tgtttctatt ttccataaat ttgttgttat cgcatctact  360

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gttgctgtga agatcttaag accttgcaat tgggtttttt tggacggtaa agctcatact  480

gattacagaa aatcattaaa cggtcttttc actaaacaag ctttggctca atacttacct  540

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aactacgagc cccaggtctt tttccatgaa atgagagaaa ttctttgcgc cttatcattg  660

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tatttggtta cagcagcatt ggaattagtc aacttcccaa ttattatccc ttacactaaa  780

acatggtatg gtaagaaaac tgcagacatg gccatgaaga ttttcgaaaa ctgtgctcaa  840

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aagatcagag aagaacaatt ggctgttcgt aacaatgaca tgtctaccga attgaacttg 1140

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accgcaccaa agggcgctat gttaattcca accttatacc cagctttaca tgatcctgaa  1320

gtttacgaaa atcctgatga gttcatccct gaaagatggg tagaaggctc taaggctagt  1380

gaagcaaaga agaattggtt ggtttttggt tgtggtccac acgtttgctt aggtcaaaca  1440

tatgtcatga ttaccttcgc cgctttgttg ggtaaatttg cactatatac tgatttccat  1500

catacagtga ctccattaag tgaaaaaatc aaggttttcg ctacaatttt cccaaaagat  1560

gatttgttac tgactttcaa aaagagagac ccaattactg gagaagtctt cgaataa     1617


<210>      79
<211>      1752
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      79

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acaacgtctc aatccataga tgtctcatcc acggcttcaa tcgtccccgt gccacatgaa   180

ccaaaacatt tgcatggcct tcctatactg caatcgccct cgcttacccc tgcggagaga   240

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gcccttcgct accacattat tacgctgctc ttggttgcat ttgtgctcta ccctgtgtcc   360

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attgcttcca ttgaagcgcc acctctgctt cctcaagaca tacccgtttt ccgaatcttg   900
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78

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<211>     5607
<212>     DNA
<213>     Saccharomyces cerevisiae

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gaggataata atgatgctgt taattctata atggcactca aatttgtatc tataaaattc 1560

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80

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81

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82

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<210>      81
<211>      2844
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      81

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gctgatgatt ctgactcaga tgaagatata gaccaattga ttgatgaact acaatctaac  240

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caaagggttg ttcctgaaaa ggacctttct acggaccctg cgtatggttt gacttcggat  360

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83

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84

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<211>      1062
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      82

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gcggaagaac tttgtcaaat tataaatgaa aaatatcaca cattttgtc agagcatcca   180

aatgttattg aggttaatga taggttgaaa cctatggtta acctagtaga ctctttaaag   240

acgctccagc ccaataaagt agctgaaatg attgaaaatc aggggctgtt taaagatcat   300

gttgaggatg ttaattttca accagtcaag tactcagccc ttacatcaaa taatgaagaa   360

tgtaccgcag tagttgccag aggtggtact gcgaatgcca taagaatcgc agcagttgat   420

aatccagtca atgttaacaa gttggcccag gatagtatca atatagcgca aatagtccca   480

atggatggtt ttcacttatc tcgcagatgt ctagacctat tcaaagaccc acaaactgcc   540

cataaaagaa gaggttcgcc ctcaacgttt gacagtaaca atttcttaca attgtgtaaa   600

attctagcca agacgtccct atgtaaggtc tcctcacatc ataaatttta ctccacttca   660

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ggatttaacc atgcactaaa agacccaact ccagatcagt actgtatttc caaatttaca   780

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tacaaaacat tagctgatac gggagcactt cttgtttata agattgacat agactatgag   900

gccaccgaag aaagggtggc caaaaggcat ttgcaatcag ggttagtcac gactattgca   960

gaaggacgag agaagtttcg cagcaatgat ttgttgaatg gcagggatat agataatcat  1020

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<210>      83
<211>      534
<212>      DNA

85

<213>        Saccharomyces cerevisiae

<400>        83

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gacacacaga acagagagga ggtggaactg atggtgaagg ccactcagtt ggccaagcag   360

acaggcacca ttgtcaacga tataaactta gagaacacca gcgctgaagt cgccctgtcc   420

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<211>        411
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        84

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agtgctaggg caatcttcaa attgttcgct aactgcaaat gggcaggatg tttcttcgat   180

ttatcaaagg aaatgaggaa agacatgctt gttgtaaatt ccgctttttt tttcaagttt   240

tattcctcca caaagatgca tatcaggaag caaatcatca ttaacattag acatcgaaga   300

aaatttgtca tcgtcttttt ttttttttcg ttttctcttt cgataagttg cgtacagaaa   360

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<210>        85
<211>        462
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        85

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86

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cgaggcgcac gcttcatagt gcctatacct ttttattgca tttccaaggc acaagaatgt 360

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<210>      86
<211>      1995
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      86

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87

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<210>      87
<211>      2301
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      87

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gacggtgccg aggatgttaa gaaacatggg tcgaagatgc tagtggggcc caggccgcca 180

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tctttatcct cctctttttac actagttgcc aacaatccag ccccaattcg gtactctcag  1920
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89

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<210>      88
<211>      1971
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      88

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gatgatgatg atgatgatga caatgataaa aaagacgatc ctttaattgt acctagtgga   420

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acaccaataa agaacacaaa tagaaagcca gtaagcatgg ataattttaa cgattcgttg   780

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<210>      89
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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      89

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cgtttaggcc gaacgcaaat ctcaaggcgc ctgcagactg cgagaagatt aaatcccgaa    300

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91

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<213>      Saccharomyces cerevisiae

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tcaaagaagc ccgcttcggc tagtagctct tcccacggga ctactcacag ttctgccagc  180

agtaccggat caaagtctac aactgagaag ggcaagcaat ctggtagtgt tccctcgcaa  240

gggaagcatc atagtagctc tacatcaaaa acaaaaacag cgacgacccc ttcttccagc  300

agcagtagca gtagaagttc aagtgtcagt cgctccggtt caagctccac aaagaaaaca  360

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aaggacgaca aaagcacttc tggtgaagat catgcacatc ctactttgct gggggcagta  540

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gaaaatggta atagtaataa taacaatatg aatattaata ctagtaatac tcaggatgca  660

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cgtgaagaaa attggagcaa acttgaagaa tatgtaaaaa atctaaggat taacaatgat 2160

aaggaccaat acacaatcaa aaacccagaa ttaagaaaca gtttcaacac agcaagtgag 2220

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<211>      3423
<212>      DNA
<213>      Saccharomyces cerevisiae

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agcactaaag ttacaactag cccagaaatt attgtcagta gttctagcac attagtttct   180

tctgttgtac ccgagtttac ttctagctcg tcgctctcct ctgatacaat tgcctcaatt   240

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93

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agttcaagca cgtccgatgt ttcttcccta ctatcaagta cttccagccc cgcaagctct 720

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tacaattcga ccgtttctac cacaacatcc gccgcatcta gtacacttgg atctaaggtt 1560

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ccaacaggca catttagctc catgagctct catacttcgg tgataactcc cggcttttcc 2040

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94

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gtaacatcga ccacaagtgg agatgaggca gaacatacca ctagcactaa aataagtaat 2820

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tag                                                                3423


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<211>      1308
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      92
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95

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acttttata catttctttc acaattccca tatgccatca actatctgga cttttgggtt   180

gaccttatga cacatacacg actttgcaaa aactacatag agttggtaag aaaatcatta   240

atcaactttc cacaagaaca acagcagaat ggaagtacat ctacggctac atttgacttg   300

ctgaacgcac tgatagaaga agggcaccta gacccggaag cacctgataa actcttagaa   360

aatagcggcc cagacgtgcc cttttcacca aaattaaacg aattgctggg tgattggaag   420

caccaatcgg gtatcggtca agaagccctg agaaacgaag acgtagcgct gatcgtcgac   480

gagataatga aaaggcgctc ccaacaagac ggaaaaccgc agataactac aaaacaactg   540

ctgcacagcg cagttggtct ctgcaacacc tatttagtat cgcccgaaca aagcgaacgg   600

tacctgagca acatccccat ggaaacgcgg aaccgcataa tagaaagcgt acaaatcgag   660

cgaaagtacg acattgagat ttttgacgac ctaaaaaacc taacttacca attcctagaa   720

atggattgtt tcccaaaatt tctaagccgc gtcgcactac acaacatcca cgatgaaata   780

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ggtttgctct ggctaggcat cggcttttgg atcggatatg ttctaatctt cctggcgtat   960

agtcgcgcaa tccgtgtcgt tacggtcgtg ccatttacac tgggatgcta ctgcattgtg  1020

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cacagacaca aaaacgctgg caatgacgaa ggagatgctt ctagtgatac cgatcacgtg  1140

ccaatgatac ttgcggtgtt cggcggtagg cgccgtctta cccgcataga gcacccattt  1200

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<211>      372
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      93

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attgtagaat acccttctgc tacactatta acacagaatg tgcgtcaaac cacaccacac   180

aataaacaat gcactttgct actaaaacca ttctattcac cttgcgaaaa caacaagcga   240

aaaaaaaaaa gcgagggcga aagagtaaga tcaccacgca cgtttagggg atcggagagc   300

ttatctatac agcaactaga agtatataga acaacaatgg tcgaacgacg ggttagtttc   360

acagctcaat aa                                                       372


<210>       94
<211>       873
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       94

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agtatattcg ggactagagg atattttgta ttctcaagtg agcaatccta tgacaaattc   180

aaacagacaa actttaatat cagtactcta gatgcggatg gtgtaggtgt tcctcttttt   240

catattgtcc aaagttataa cgttattggc aaaattactc ggagctcgcc ggatttctat   300

atctacaagt acgttttaca aggggtgcaa gatccgcctt tatactctga ttgtaaagtt   360

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gacaggctca attactcaaa tagtaaccaa aaggaaaggc aaaaaccaga tcaaggaaaa   660

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agatccacgt caaaatgctc caatcttatt attggagaac actcaaagcc agactctctt   780

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<212>       DNA

<210> Saccharomyces cerevisiae

<400> 95

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ttttatgata agaagcgcat ttcattagat catgatcacg ttaaggtttg gtggtaccag   180

gtttcttttg aacgtggatc ttcccctgtt tccctgata agaggccatc ttggaaatct   240

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actgccaagc agaataagac accagaatat tacggctccg gtttaatgtt gtacggaaag   1500
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aagtccaact attcattaaa tccaagggat gaacaaagta ttgtggtaag ggtttacgaa 3060

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99

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ttgtatttct ga                                                   3252


<210>      96
<211>      1704
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      96

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<213>      Saccharomyces cerevisiae

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102

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<213> Saccharomyces cerevisiae

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<213>    Saccharomyces cerevisiae

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105

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<213>      Saccharomyces cerevisiae

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106

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<212> DNA
<213> Saccharomyces cerevisiae

<400> 104

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tcctcactat ggttaaacga cagttctagt ggcagcttaa taaattactc aataaatgct  1140

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agcataagga tagttccatt tggctttcaa aacaatccaa ttagtaggga gaagtgcctc  1260

aaagacttag aggatttcga tattgaaatt gcaaacaggc ttggaatgat cgaaaaagtc  1320

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109

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<211>      1485
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      105

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gagaagaacg accatccgct caagggaaat gatgaggcaa tcaaaatgct gtttactgca   180

atggatgtta acaaggactc tgtagttgat ttaagcgatt tcaagaagta tgcttccaat   240

gccgaatctc aaatttggaa cggcttccag aggatagatt tagatcatga cggtaagatt   300

ggcattaacg aaataaatag gtatttgtca gacctcgaca accagagcat atgtaataat   360

gaacttaatc atgaactttc aaatgaaaag gtgaacaaat ctcgaggtt ttttgaatgg   420

gcgtttccaa agagaaaagc caacattgcg ctacgaggcc aggctagcca caaaaagaat   480

actgataatg atcggtcaaa gaaaaccacc gactcagatt tatacgttac atatgatcaa   540

tggagagact ttttgctgct ggtaccgaga aagcagggtt cgagacttca tactgcttat   600

tcctattttt acctattcaa cgaagatgtc gatctgtcct cagagggaga tgttactctc   660

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tcaaggactt gtaccgcgcc atttgataga ctgaaagtgt ttctcatcgc aagaacggat   780

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gctcagtttt ccgtttatcc tatagatact ttgaaattca gggtgcagtg cgctcctttg  1140

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gggtgcattc agtggaactg taggagcttc tgttgtttat ccaatcaatc ttttaagaac 1440

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<210>      106
<211>      2316
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      106

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gaatggtact ttggtgaata ccaggattca aatggcgacg ttattgaggg tatcttcccg  180

aaaagttttg ttgctgttca gggatctgaa gttggaaagg aagccgaatc atctccgaat  240

accggttcca ctgagcaacg tacaatccag ccggaagtag aacaaaagga cctaccagag  300

cccatttccc ctgaaacgaa gaaagaaact ctgtccgggc cagtgccagt tccagccgct  360

acagtgccag ttccagccgc tacagtgcca gttccagccg ctacagcagt atcagcacag  420

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tccctaaagg aaaacgaaaa aagattgtt cccgaaccaa ttaatcgtgc acaggtggaa  720

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gagccctata cggaaactga gaagcagaa gaaatgaaa aaactgaacc gaaacctgaa  960

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<211>    309
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    107

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gagctatcga ttttttctgc ataccaagca agtttacctg gcgaaaagaa agtcgacaca   180

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ccaagttga                                                            309


<210>      108
<211>      3093
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      108

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cctcagtacg gtccaggttg cacgcctggt aaaattgtac attgtgtcct ggatgattca   180

ctgcccttct gtagcattgt tgtaccttcc aaacttttg ggtttatgcc gacacagccc    240

actatggatt tttgctattt tgaacccata ttagacaatg tagtacctgt actggatagc   300

gtaacgtttc tgattaatga acaattgtac tcaaaactaa tggacctacc gcaagagatg   360

caacaaatac aattttgca ttacaaatat aacatcaact ccatggaaac cgtggttcat    420

tctcgagata ttttaacatc tggtctttgc caaattttaa actgctcacc tttcccgcag   480

ggccttgttg attttacaga aacccaattg atattagtaa atgatactga gcagaaacta   540

agtgctctaa aatatgctaa cgaagatgaa gaatatgcat tacctaaaat agggacaaat   600

tctgctttat caattgatct tgaatctctc ccctgcacaa tttcaagaga tcttttgcga   660

cctgcacctc acatcaatga tgataattca atatatgcct ttacagacgc tgaaactcta   720

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ataggccata cagatattcc cattgctaat caagttttca tctcaagagt tggaggctgg   960

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113

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114

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<211>     1626
<212>     DNA
<213>     Saccharomyces cerevisiae

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agtactcctt tcgaaaagtt agaacctgcg aaacagaacc atccacagaa agactgctgt  180

gctaccgaaa aggacgatct ggttgacgtg agcgaattat ttcccaaaca gaacaacaaa  240

caattgagtc taacatcaaa atcttcagtt gtaccctgtg ctttaaattt ggataaccta  300

gaaacacctt tctcaattaa aattgataat aatggtgcag tcactacaca gttgaacttg  360

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ccctctaatt tccttccaat cacgcccgta agtagcgtaa tcactcctgc atcgaagaaa  540

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cgacacataa aaaagcatgc gaaaaggaag gcctatcact gtccattttt tgataatagc  720

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115

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caaactacac aatcaagagg acctacagaa gtccaaaatc tcaaagagtg gtcaataata 1260

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aatatgattt ccattaatga gatgttacag aagcaaatgg actttgaact tctgggtgag 1560

aatcatttga aggagactca agattatctg ccctttaca aaaaagctta tgggatagaa 1620

ttttaa                                                            1626

<210>    110
<211>    1770
<212>    DNA
<213>    Saccharomyces cerevisiae

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116

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tctggtccta atgctaaacc atggtttttac ttgaacgagt ctttcaggga aggaattaac  1440

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tttagaaagg cacacaagga tattactgtg tatggatatg attttgagtt tattgatttg  1560

gacaataaga aactgttcag cttcacaaag aaatacgaca caaaacatt gtttgctgct  1620

ttgaacttca gctctgattc gatcgacttc acgattccaa acaatagctc atcgtttaag  1680

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<210>    111
<211>    2115
<212>    DNA
<213>    Saccharomyces cerevisiae

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tctctagata tcaaaaacac tgtcttagat agtgcggatc tcaatgacat tcaaaatcaa  180

gaaacttcac tgaatttggg gcttcctcca ctatctttcg actctccact gcccgtaacg  240

gaaacgatac catccactac cgataacagc ttgcatttga aagctgatag caacaaaaat  300

cgcgatgcaa gaactattga aaatgatagt gaaattaaga gtactaataa tgctagtggc  360

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aataccacta ctatgaacgc aaatgcagac tcaaatattg ctggcaaccc gaaaaacaat  1080

gacgctacca tagacaatga gttgacacag attcttaacg aatataatat gaacttcaac  1140

gataatttgg gcacatccac ttctggcaag aacaaatctg cttgcccaag ttcttttgat  1200

gccaatgcta tgacaaagat aaatccaagt cagcaattac agcaacagct aaaccgagtt  1260

caacacaagc agctcacctc gtcacataat aacagtagca ctaacatgaa atccttcaac  1320

agcgatcttt attcaagaag gcaaagagct tctttaccca taatcgatga ttcactaagc  1380

tacgacctgg ttaataagca ggatgaagac cccaagaacg atatgctgcc gaattcaaat  1440

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gaacaaaatg ctaattctac tccaaatttc gatctttcca tcactcaaat gaatatggct  1620

ccattatcgc ctgcatcatc atcctccacg tctcttgcaa caaatcattt ctatcaccat  1680

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gaactcgagg agaaaccgtt ccactgtcac atttgtccca agagctttaa gcgcagcgaa  1980
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118

catttgaaaa ggcatgtgag atctgttcac tctaacgaac gaccatttgc ttgtcacata 2040

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catggagaca tttaa                                                   2115


<210>    112
<211>    375
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    112

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agaatcaaaa agatcagtag agaaacgcct gtccagataa gtttctggtt gtatggaacc   180

ttcctttctg gagcaatcac ttccggcagg aaagattcaa atggcttaaa caagtctaga   240

acacggttgg aggacatttt caaagtaaag cgtgaaccag tgtcagtttt tctacttgct   300

actatattta actatgtttt tttcttttgc tttcaccaac tgaaccttgt agtaaatgga   360

gtgaggttga attga                                                   375


<210>    113
<211>    1098
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    113

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ctgcccgctt cgttggcagc taatattcct gtcaagtggc agaaattgct agggttgaac   120

agtgggttca gcaattctac gattttgcag agactttga actccaagaa tgccgtcaaa   180

gaatgtagaa ggttctacgg gcaggtgcca ttcctgtttg atatgtcgac gacgtctttt   240

gcatcgctat tgcctcgttc cagcatcttg agagaattcc tctcactatg ggttattgtt   300

acgatctttg gtttactact ttacttattc acggctagtc tcagctacgt gtttgtgttt   360

gacaagtcga ttttcaacca tcctcgttac ttgaaaaacc aaatggcaat ggaaatcaag   420

ttggcagtca gtgctatccc atggatgtcg atgttgaccg ttccatggtt tgttatggaa   480

ttgaacggcc attctaaact atacatgaag attgattatg aaaaccacgg tgtaaggaag   540

ctcattatcg agtacttcac tttcatcttt ttcactgatt gcggtgtgta tttagcgcac    600

agatggttgc attggccaag ggtctaccgt gctctgcaca agcctcatca caagtggctg    660

gtctgcacac ctttcgcatc tcattctttc catcctgtag acgggttttt gcaatccatc    720

tcgtaccaca tctacccatt gattctgcca ttacacaagg tttcttattt gattctgttc    780

acttttgtta acttttggac tgttatgatt catgacggtc aatacctatc aaacaatcct    840

gccgtcaacg gtactgcctg ccacacggtt caccatctat atttcaacta caactacggt    900

caattcacca ctctgtggga cagactaggg ggttcttacc gtagaccaga tgactcattg    960

tttgatccta agttaagaga tgctaaggag acctgggacg ctcaagttaa ggaagttgaa   1020

catttcatca aggaggtcga aggtgatgat aatgatagaa tctatgaaaa cgacccaaat   1080

accaagaaga acaactga                                                 1098


<210>      114
<211>      1659
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      114

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gcacctactg ttgactgcaa acagtacgaa gaattcggtg attctaacga ttacaaaaat    120

gatgatgtgg tcagagtagt cagccatagc gatgagagta ctgatgacga actttgtaat    180

gtgaatttaa cagaaacagg ggcaatcttc acgagtaaag gttttaccgg gttaagcaaa    240

ggtttcacag ataagaccct ggatttcctg gtacgagtgg ccggttcgca ggcggttttt    300

tttattgttt ggatcatcct cataatttgg gtggttattg gtattgttta taacgcacct    360

ttcaattggc aagttgttat gcaggacgga cagtctattc aaagttatgt ttgggacaca    420

ctgttgatga gacaacagtt gatgagtacg catgaacaaa ttttgatctg cggtagattg    480

aagtcgagat tggcttcctt caaaaactat ctaacaagaa gcaccccaga ggaagaaaaa    540

gcagactgca cagttgaagc taatgaagtc agctctgttg aaaatcatat agacccatct    600

gccattaacg gagaactgcc tgtggaaaat tggtacgacc gtttatctaa cgtagcaagt    660

aggtatatgg gttcaattgc agcaatggtg atattttgga taggtatttt cgtttggatt    720

ggttgcggtg ctatcccaaa agatgcgggc aacactccac cttacaccgg agaaactaca    780

ggtagtaatc caagattgaa aaagttcagt gacgcttggc agatgtatat taacactgca 840

gttgcagttt cccttctaat ttgcactact ttcttacaaa atataagggc tagacatgat 900

tatttcacgg ggaggttttt agttgatatc tttgatatgg acgagaaaat cgactatcgt 960

ataagaaagc attttaacga ttttgaaaca cctcacccag ttgttactat tgaatctaaa 1020

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ggtttcgttt tgagagaagt gtacttccga atcgttcaac atgaagagaa aaattattct 1260

gatgtggcta agaagacct tgaattattc caagaattag gtattgaatg tcccgaagaa 1320

tttagtggta aagctcctga aattaacact attggttaca gaacatccca atatattaat 1380

aggatctgct caactccatg gagtgttctt gtatccgtca tcatcatcat tggtttaatt 1440

tgtattgctt ccggtttgcg ttggagtaca acaggtcaat tgattgctaa cacgccaact 1500

atgattatcg aagaattttt cttgctagtt ttgttgcaag cacataattg ggccgatcgt 1560

caaagaagag tggaggttac cgctttgtac gcacgtaggc gcatacttct atcatacgta 1620

gaaaagcgtt tcccagaggt tatgatgttg gaaaaatag                         1659


<210>      115
<211>      1722
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      115

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ttgcgtgact ttgcaaaacc taatcccgct gacacatttt ctaatcttga ttctggtcat   180

tgtcctttgg tcacaactcc aataaaatat gagtgcccag atggaaagag ttcttttttc   240

cgaggagaca ctaaatttga aaccctgttc agtaatagaa aattctatga gttcaaagat   300

aatttgaaaa ggggattgaa gaaaatacgt catgggagaa acggacatca aagcgaaaag   360

agatgtccag ttgttgaaga aacaaaaaag tctgtgtcag ataatctgga caaaccagac   420

aataatacgc cctgtttcga cagattccac acaaattcga agaatttga aacgcaattt   480

121

gatcattcaa ataggagcca aaattccgag aaggcttatc tagacaatga atcctgttgg 540

aacctaagtg agaaatttat tcctttaat aatttaaaat atgaagattt gaaacatttt 600

gaagagaatt tgcaaagctt agcgcctgca actttactc caattgaatc aaatgaatcg 660

cttgataggt cagattcgac acgtggcaca aaacgaagca ttcgcaatga ttccagtgat 720

acaacatctg aaaagaggct atgcttaaaa caatactcag atgaacctga atcggatcat 780

tcgatggaaa gtacaccatc catttacatt accaagaag ttcaagaaag aattgaagca 840

ttaagctcca cggattcgtt tttaattgaa aaagtagatt ttccctctaa caaaattggt 900

tccagtgcct ccgattatga aagtgataac gaatacagaa atatggatga ggattcaata 960

aacgatgtta ccactgagaa agagggaaat gtggtcatac cagactctaa tactagcacg 1020

gtggacgcaa tggaaaaacc aattgaagtg agctcggcct taaaagatga tacattggat 1080

aaagacatag atgatgcgag cagtagctat tcggatgatg tagagaccac attcgagcca 1140

gttgaatctg aggaactttc cgatttatct gatacaagct caagtggaag tagtaaaatt 1200

tatactatcc ccacatttcg cggccttact aataggacca atatatcaca aattctttca 1260

aaagttggta aagctgattt aagccaagat aacttaacgc atttgatcaa aagtcatcaa 1320

aaaaagaaaa gatgcgtgaa ttttagaaat aaaagattct atgatgcttt caatccatat 1380

gttgataacg aagaagatgc agagttatct gacagcgaaa acatttcaga aatggataca 1440

gatctttgta taaaggatcg gagtacctca agtgttaggt ttgatgaaaa ctcacgtctt 1500

ttaatctaca aaaaatctaa aaagttaaac aaagatgaga ctcaaagtgg ttattcgact 1560

actgaaatga ggtcaattct aaagacaaag atgaattcac agcatgatga ggagtctcag 1620

agagcttcga agtgtgacac agtaggtgta gcccaatttt tacattattt tcaatataca 1680

gagtataaaa ggcagagaaa tgaagcagaa attatagact ga 1722

<210>    116
<211>    618
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    116

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gcatctacca catgtggctc agggttattt atgctcactt caagcgtgcc attgttacag 120

122

gaagtgtgcg acgcgtcggg tacgctagca tgcaccgctt cattgttcac aagcagcggc    180

ggctttttta gcaaaccacc tgtagttcca ctagattttc tacttctgct tctacttcta    240

ctattaccgt tgctattgcc accgttgccg tccgttaaag gtgagccaga cgcatgcgag    300

attcctgtac tgcctccgtt gttatttttt ttgttgttgt tgctctgcgt tcttccagag    360

ccacttgaaa cctctttttcc attcatatcc gcgatgcaat cccttatacg cttcttaata    420

aactttgctt cccactcttt cactactgac catcgatcct tcttatttca tagcctcacg    480

agcacaaatg ataatacgag aaaaaggccc gaccgggtaa ccaacccttt tactatctct    540

cgctctacct ttagtaataa tgtcgtctat ataaggattt actcatacag tagtccaaaa    600

tataccttttc cgtgctaa                                                 618


<210>      117
<211>      534
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      117

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tacgtaaagt ctttcccacc attcttgcct tggccgctgc aagatccgct cttcgtggtc    120

tcgttactaa gagtagatat agtcatttct atttgttacc acacacaaat atatcttcat    180

ccggctgata tttgtctcta ctgcccctttt gcttgcaatt taatgaccaa attacacatg    240

ttagcttcaa gaaaaatgat gtaccatcaa aatgtctcct gcaacgaacc ggggcaccgc    300

gccggcagag tcaggaaagc gagatcgaca ctgatagtga taaacagcaa cacaatggag    360

cgattaccat tcactcggaa cggatccgga caacagtcaa ataaactccg ggatcccaaa    420

aagggccgta cacacaaacc caagccgagc gaaaaacaca aaaaaaataa aacagggaaa    480

aaaggagcgc aagagaaaac gcacaggagt aggagcagca gaaagggggaa ctaa          534


<210>      118
<211>      1833
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      118

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123

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tccgcagaag ccaacaaacg gcattcggtc acgtacgata acgtgatcct gccacaggag  120

tccatggagg tttcgccacg gtcgtctacc acgtcgctgg tggagccagt ggagtcgact  180

gaaggagtgg agtcgactga ggcggaacgt gtggcaggga agcaggagca ggaggaggag  240

taccctgtgg acgcccacat gcaaaagtac ctttcacacc tgaagagcaa gtctcggtcg  300

aggttccacc gaaaggatgc tagcaagtat gtgtcgtttt ttggggacgt gagttttgat  360

cctcgcccca cgctcctgga cagcgccatc aacgtgccct tccagacgac tttcaaaggt  420

ccggtgctgg agaaacagct caaaaattta cagttgacaa agaccaagac caaggccacg  480

gtgaagacta cggtgaagac tacggagaaa acggacaagg cagatgcccc cccaggagaa  540

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gccatcaggt gctgcacaga ttactatgcg tcgtacggca gtgcatggaa taagctggaa  660

atcgtgcagt acatgacaac ggacttgttc acgatcgcaa tgttggactt ggcaatgttc  720

ctgtgcactt tcttcgtggt tttcgtgcac tggctggtga aaaagcggat catcaactgg  780

aagtggactg ggttcgttgc agtgagcatc ttcgagttgg ctttcatccc cgtgacgttc  840

cccatttacg tctactactt tgatttcaac tgggtcacga gaatcttcct gttcctgcac  900

tccgtggtgt ttgttatgaa gagccactcg tttgcctttt acaacgggta tctttgggac  960

ataaagcagg aactcgagta ctcttccaaa cagttgcaaa aatacaagga atctttgtcc  1020

ccagagaccc gcgagattct gcaaaaaagt tgcgactttt gccttttcga attgaactac  1080

cagaccaagg ataacgactt ccccaacaac atcagttgca gcaatttctt catgttctgt  1140

ttgttccccg tcctcgtgta ccagatcaac tacccaagaa cgtcgcgcat cagatggagg  1200

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gcggagttga ccaggtttgc ggacagatat ttctacggcg actggtggaa ttgcgtttcg  1500

tttgaagagt ttagcagaat ctggaacgtc cccgttcaca aatttttact aagacacgtg  1560

taccacagct ccatgggcgc attgcatttg agcaagagcc aagctacatt atttactttt  1620

ttcttgagtg ccgtgttcca cgaaatggcc atgttcgcca ttttcagaag ggttagagga  1680
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124

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tatctgttca tgttccaact gtcgcagttt gtgtggactg ctttgagcaa caccaagttt 1740

ctacgggcaa gaccgcagtt gtccaacgtt gtcttttcgt ttggtgtctg ttcagggccc 1800

agtatcatta tgacgttgta cctgacctta tga                            1833


<210>      119
<211>      3363
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      119

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caggcgaccc ctgaatgcca aaaagtttcc tctaagtatg atcctgataa cccaaacaaa  180

gataagttgg gaacatacga tggggtattt gtgcctactg ctttaaacgt attgtctatc  240

cttatgtttc ttcgtttttgg cttcattttg ggtcagttag gtattatatg caccatcggt  300

cttctgctat tgagttacac tattaatctt ctcaccacgt taagtatatc tgctatatct  360

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ccacctgcag ctttgggaga gctactacca agagggcatt ggcacgaatt tacatatgcc  600

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tgggttatat tcatgggtga aatggctact tctctttttct ccatcatagt ggggatgctc 1140

ggtgctgctt atgtattaga agcaattgca aaggataaca ttattcctgg tttggagatt 1200
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125

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caaatattgc tgtttgtaga taatccaagg acgagctgga acttaataag gttttgcaat 1680

catttgaaaa aaggtggttt gtatatttta ggccatgttg cagtaactgc ggattttccg 1740

aagcaactaa atgaattaaa aactcagcag aaagcttgga tgaagatcag agacatggca 1800

gcaataaagg cttttgtcca agttgggact ggtccctccc ttatatgggg aattaggaat 1860

gttttattg gttccgggct tggaggtatg aaaccaaaca ttactgttgt cggttttttt 1920

gacctcgaaa gttatagaaa gcacatccca caaagtcgca gccaaaataa ccttcagaaa 1980

caggtggaaa taaaagctac agtgccacgt agtacatgct ctgatgtcaa aatcaatgtt 2040

ccattgccta cggatgagtg taaaaatgaa accaaagtta atgtacaaca atgggttcaa 2100

attgtagaag atctatcact gatgcaatcc aatattgcca tagcgcatgg attcaaaaat 2160

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atccaaatgt gcggaaaagt tgaggcaaag ggtgaccagc ctgcggctat cactactaac 2280

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aagcgcacac attcgcttcg agttatttta tttgtggaac aagaatatca tagaacgaac 2400

gaaactcaac gaatgaaaaa gctattacag gttctaagaa ttgacgcaga ggttttggta 2460

gtatctttag atcaattcag agtatacaac acaattgtca agggagaccc aatcgtgttt 2520

gattatgtca actcgaaatt ggccgataat gaatggtgga agatttggt tgaagctcgt 2580

gatacattaa aaccgaagcg gaggttttcc actattgaac ctcaaacgat agcaaagcaa 2640

tttacacaat caagaaaata tacgtctggg gttcagaaat tgggtgtctc atttacaatg 2700

aatacgagaa tgccaactaa ccgcattgat accccatgcg agagtgagga ctccgatttg 2760

gatacagatc ttacgtcaat tcgtgatgcc ttctcggcat cgactaatat ttcagtaggt 2820
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aaggacttaa cgaccaaatc gaagaccggt tccgacagaa caaatttact cgtaaagaat 2880

ttacaaagcg atgtgtcaac acagtcgtta agacccgttt tctcgagtaa tactttgccg 2940

aggacgagag tcgtggaaga tggcacgggt gaacagccga cactgatccc aattgccgaa 3000

cctgaccttt cgaatgggaa cggtactggg agcggtattg gcaacggcaa caaattaaag 3060

aaaccggttc ttcccgaatt atccacttgt tgttcaaaag atagtttagt cacagcgatg 3120

caaaatttag gtttcaatga tcttcccagc actgctcaac atttggttct gaatgatgtg 3180

atgacacaaa tgtcaaagag ttcggattta attttttcaa ccttgccagt tccagctctt 3240

ggaacacatg aagatcacga tgcaagttta caatatgtcg aggacttgga tatttggttg 3300

gagggcttac ctccatgcat gttaatcaat tcgcaaacca tgacagtaac tactgcatta 3360

tag                                                              3363


<210>        120
<211>        543
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        120

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gagtaccgga cctcattcgg tctcgctgtt atacctttca ccgttactga aagtaaggtc  180

aaaagaaacg tcatttcaca aattaatgac ggtcaagtgc aagtaacgac acaaaaatta  240

cctcatccag tttcgcaaat tggagacggc caaatacaag ttacaacgca gaaggtgcct  300

ccagtagtgt cacatattgt gtcacaaata ggcgatggtc aattacaaat aactacagct  360

aaaaatgttg tcacaaagtc cacaattgct gttccaagta aaactgtaac tgcgacagca  420

acttcaaccg caactgctgt ttctcagatt catgatggtc aagtgcaagt tactatttct  480

tcagccagta gtagttctgt gctttccaag agtaagttaa gagccaacaa agaaaccaaa  540

taa                                                              543


<210>        121
<211>        2808
<212>        DNA
<213>        Saccharomyces cerevisiae
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127

&lt;400&gt;    121

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atgaccattt atcaggattg tatgaacacg tttaacgaat cacctgtcaa ttccaagaga  120

tgtcgtttat tgatttctcg cttgctgaga ctcttggccc agggcgaaac cttcccacag  180

aatgaagcaa ctgcattatt tttctctatc tccaaattat ttcaacacca gaacgatcct  240

ttaaggcagg ctgtttattt ggcaatcaag gaattgagtg gcatttcgga ggatgtgttg  300

atggcaacct cttcaatcat gaaggacgtt caaaacggtt ccgatttgat taagcctgac  360

gctattagat cgctgactta tgtcttggat gaatctactg cttttttccgc tgaaaggtta  420

ttaaaaagtg ccgtggtaag tagacatcct tcaatatcct cagcagcatt atgtacttct  480

tatcatttgc tgcccatttc agaagtcact atcagaagat tcaccaatga aactcaagaa  540

gctgtttttgg atttgaaaca atttccaaat caacacggta atagcgaata ttatccaaac  600

tccacttata tttctcaata tcatgctctt gggttgcttt atcaactgaa gaaaactgat  660

aaaatggcgt tactaaaatt ggttagacat ttctctgaaa acaattctat gaaaaatcaa  720

ttggccaagg tagaattggt caagattgtc aacgatttga tttataggga tcctcaatta  780

tttagtcaat tcaggccact tttgtctgat tggctatcca acaagttcga atctgttcag  840

ttggaaacgg cgaaattgat tacttctttc gctactcgca attcccgctt agtggctccc  900

gagttatatg cggcagctat cagtgcttta cagtccttac tgaccgttcc tcgtgtttct  960

tctagattcg ctgcattgag aatcttaaat agaatatcca tggtttcacc agaaaagatt 1020

gttgtttgta atcctgaact agaatcttta attaatgatt ctaatagaaa catttctact 1080

tatgcaatca ccactttatt gaagacagga acttccaaaa atatttcatc tctgatttcg 1140

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gttcgtacgt tgtctttgaa cttcccacag gaatggaagt caatttttgaa cttcttaatc 1260

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128

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      122

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129

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gacccgtatt ctcgtttcct gccatcatct cgtattccaa aaaaatcttt ccacagtccc  300

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<210>    123
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<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    123

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aatggtgaac tcagcaagag atcgaacggc catgaaaaat ttgtactagc taacgagcaa  180

agctttttatt ctgttgagct agccattggt acaccttcac aaaacctcac tgtgctgtta  240

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130

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<210>      124
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<400>      124

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gcggcgctaa ctttgaagaa cgagctggtg tccaaggact cagtcaagac gcagcaattt   240

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gctatagcag atattgagtt gccccatggc gcatggccag agttgatgaa aattatggtt   420

gacaatacag gtgcggaaca accagaaaat gtcaagagag cctctttatt ggccttgggt   480

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gaaagaaact accttatgca agtcgtctgt gaagccactc aagctgaaga tatagaagtt   720

caagcagctg cctttggttg tttgtgtaaa atcatgtcac tatactatac atttatgaaa   780

ccttacatgg agcaagccct atatgcattg accatagcta caatgaaatc tccaaatgat   840

aaagtagctt ccatgactgt ggaattctgg tccactattt gtgaagaaga aatcgatatt   900

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gaagatgacg attggaatgt ttccatgtcc gcaggtgcat gcttgcagtt gtttgcccaa  1080

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gtcgaacaat tagcagaagc cacaccatct ccaatctata acttctatcc cgctcttgta  1500

gatggtttga tcggtgctgc aaatagaatt gataatgagt tcaatgcccg tgcatccgcc  1560

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ctgttcttca ggttgttgga aaaaaaggac tctgcgttta ttgaagacga tgtgttttat  1860

gctatttcag ctctagctgc ttctttgggt aaaggatttg agaaatacct ggaaacattt  1920

tctccctatt tattaaaggc tttaaatcaa gtagattcgc cagtttcaat caccgcagtg  1980

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gccgtcttga gcgtgttcgg tgatattgct tccaatatag gtgctgattt tattccctac  2160

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atagtagcgg gtcttcatga taaacctgaa gctctgttcc cttatgttgg tactatattc  2340

cagttcattg cacaagttgc agaagatcct cagctgtaca gtgaggatgc tacctcaaga  2400

gcagcagtcg gattgattgg tgatatagca gcgatgtttc cagacggctc aatcaaacaa  2460

ttttatggac aagactgggt tattgattac attaaaagaa ctaggagtgg ccaattgttc  2520
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132

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ttataa                                                          2586


<210>      125
<211>      321
<212>      DNA
<213>      Saccharomyces cerevisiae

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ccccagttac cagatccaat cacagtaacc ttgaaaggct tttcggcagc cttcaaagaa  180

acagaagagg aacttctctt tctaccagca ttcaagtggc cggaagttaa gtttaatcta  240

tcagcagcag cagacatctt tatattatca atatttgtgt ttgtggaggg ggggggtgta  300

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<210>      126
<211>      1482
<212>      DNA
<213>      Saccharomyces cerevisiae

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tcagcaatac acctgcaaat ttccaacaaa tctactccca atacattcaa ttctttagat  180

ttttctacga ggtccaggat aaatggttct ctgagttatt tatactccga tgcacagcaa  240

ttggagaaat tcatgcgcaa ctctactgat atcccattac aagatgccac cgaaacatac  300

agacaattgc aaccaaacct caatttcagt gttagtagtg cgaatacgtt gagtagtgac  360

aacaccacag tcgacaatga caagaaatta ctacatgact cgaaatttgt taaaaaatcc  420

ctttattatg gtagaatgta ctaccccagc tctgatttag aagcaatgat aataaaacga  480

ctaagtccac aaacccaatt tatgcttaag ggtgtcagta gtttcaaaga aagcttaaac  540

gttttaacgt gctatttttca aagagattct caccgcaatt tacaggagtg gatattttcc  600

accagtgatc tattatgtgg ttatagagta ttacacaatt ccttaccac gccttccaag  660

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tattcgattg aatcaaatct ttcatttggg tgcgaatttt ggcaaaaaaa gcatcatttg    960

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gaaaaatttg ataacaaaat aaatagttcc atttttacca gtgtttggaa attaagcacg   1260

tcattacgtg acaagacttt aaaactatta tgggaaggca aatggagggg attttaata   1320

tctgccggga cagagctggt attcactaga ggctttcaag aaagtttatc cgatgatgaa   1380

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<211>     1017
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     127

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tctggctcag taactatcac atcttctgaa gctccagaat ccgacaacgg taccagcaca    180

gctgcaccaa ctgaaacctc aacagaggct ccaaccactg ctatcccaac taacggtacc    240

tctactgaag ctccaaccac tgctatccca actaacggta cctctactga agctccaact    300

gatactacta ctgaagctcc aaccaccgct cttccaacta acggtacttc tactgaagct    360

ccaactgata ctactactga agctccaacc accggtcttc aaccaacgg taccacttca    420

gctttcccac caactacatc tttgccacca agcaacacta ccaccactcc tccttacaac    480

ccatctactg actacaccac tgactacact gtagtcactg aatatactac ttactgtcca    540
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134

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gaaccaacca ctttcaccac aaacggtaag acttacaccg tcactgaacc aaccacattg   600

actatcactg actgtccatg caccattgaa aagccaacaa ccacatcaac caccgaatac   660

actgtagtca ctgagtacac tacttactgt ccagaaccaa ccactttcac cacaaacggt   720

aagacttaca ccgtcactga accaaccact ttgactatca ctgactgtcc atgtactatt   780

gaaaagagcg aagcccctga gtcttctgtc ccagttaccg aatctaaggg cactaccacc   840

aaagaaacag gtgttactac caaacaaacc acagccaacc caagtctaac cgtctccaca   900

gtcgtcccag tttcatcctc tgcttcttct cattccgttg tcatcaacag taacggtgct   960

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<210>      128
<211>      1386
<212>      DNA
<213>      Saccharomyces cerevisiae

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aaagcggttg ttcaaagtta cggtgttagc aaggaggctg atatgggcaa tgataaaata   180

cacaaaaata gcgtgaaatt gcaaaagaag ctcgctaaac tgttcaagga atcgaaaaac   240

gttgtcaggg tgccctctat agatctagaa tcaattgaga atatgtcaga agaagatttt   300

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gaggataata cctactatta tttcactaag gatcccaata tactaaagca aatcctaccg   900
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135

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gccaagaatt tatcttatac atcttcaagt gaggaagaag atggaatcaa agaagggata 1200

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cattcttcgt tcacaagcac ttcttgcgag tccgataacg aatgttctaa gatttccaac 1320

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<210>      129
<211>      2280
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      129

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gcacaggccg tcttaaacaa gagaattggt gaaaatactg ccagggaaga ggaagaggaa 2220

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<210>      130
<211>      1863
<212>      DNA
<213>      Saccharomyces cerevisiae


137

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tcaaagacag atgatgtttc aaggtcttct tctagatctt caaaaaagaa tacagattct   180

gaccaagagg atcaaataaa gtataacaaa cccaacgacc gaagatctac cataggaaag   240

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cataattctt caagcggtag tgatgatacc tcatcaagaa agaaaaaatc cttgagatta   720

acaagatttt tcaaaaaaat tcataatgat tatcacgata accatcatca tcaccaccat   780

cacaaccgtg gatccacccc tacaaaaccg aagctcaatt tgaacaccaa tgaaaatata   840

gtagaaagta acggaaaagc gttatacgaa acagataacc cagtggagct attagaaaaa   900

tatggtattc ctggtagaaa attaggcgaa ggagcttccg gttcagtgtc cgtagtagaa   960

agaacagacg gcaagttatt tgcttgcaaa atgttcagaa aaccacactt aaacaatgaa  1020

ggaactaatc agtctcaatt agctaattat tctaagaagg ttaccactga attttgtatt  1080

ggttccacgc tgcaccacga aaatatcgtt gaaaccctag atatgttgac tgaaggtgac  1140

acctatttat tagtaatgga gtatgcgcca tatgattttt ttaatctcgt catgagtaac  1200

ctaatgacac aagatgaagt caactgttac ttcaagcagc tgtgccacgg cgttaattac  1260

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gatggcatct tgaaactgat tgactttggg agcgctgtag tgttccaata cccttacgaa  1380

gataccattg taaaatcaca tggaatcgtg ggttctgacc cttatttggc tcctgagtta  1440

ttgaaacaaa catcctacga tccaagagta gcagatgtgt ggtctatcgc tattatattt  1500

tactgtatgg tccttaaaag atttccttgg aaggctccaa aaagagctt caactcattt  1560
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138

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aagcaaagag ttttaatgaa tgacgtggta aaggatgatt ggcttgtatc cgtcccctcc 1740

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taa                                                                  1863


<210>        131
<211>        1089
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        131

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tcggaatact gtatatccag tgacgcagga acagagaaga tggatagcga cgaggagaag  180

tcgttggcca atctgccgga gttgaaatac gctcccaagc tatccagcct ggtgaagcaa  240

gagacgctca ccgagagctt gaaaagacca cacgaagatg agaaagaggc gatagatgag  300

gccaagaaga tgaaagtgcc gggagagaac gaggacgaaa gcaaggaaga ggaaaagagt  360

caagaactgg aagaggcaat tgacagcaag gagaagagca ccgacgccag ggacgagcaa  420

ggggacgaag gtgataatga ggaggaaaac aacgaggagg ataatgaaaa cgaaaacgag  480

catacagcac cgcctgcgct ggtgatgccc tcccccatcg aaatggagga acagaggatg  540

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tatgacaatc aattggtgcg gttgcaaacg gagctgcaga tgtgtctgga agggtcacac  660

ccggaattgc aggtctacta ctcgaagatt gccgcgatcc gtgactacaa gctacaccga  720

gcgtaccagc gacagaagta cgagctttca tgcatcaaca cagaaacaat cgctaccagg  780

acattcattc accaggactt ccacaagaag gtcaccgacc tgcgagccag gctgctgaac  840

agaaccacgc agacctggta cgatatcaac aaggagcgcc gcgatatgga tatagtcatc  900

ccagatgtca attaccacgt ccccatcaaa cttgataaca gacgctgag ctgtatcacg  960

ggctacgcag cgcacgacag ctgtgctatc ccggcgagcc cgtggcagag gacctcgctt 1020

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accgaatga 1089

<210>    132
<211>    984
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    132

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aaagatagac tgacagcatt gcaaacggat ttaacttctc tgcatcaagg tgataatggc    180

caatatgccc gccaagtacg agatttggag gaagaaagag atctagagtt agtcaggttg    240

cgcctgtttg aagagtaccg tgtttctcgt tccggtatcg aatttcaaga agatattgaa    300

aaggctaagg ctgaacacga gaaactcatt aaattatgca agaaagact gtattcgtct    360

atagagcaaa aaataaagaa attacaggag gagaggttac taatggatgt ggccaatgtg    420

cactcctatg ccatgaatta tagcagaccg caataccaga gaacacgag aagtcacaca    480

gtaagtggtt gggattcttc gtccaacgaa tatggaagag atacagcaaa cgaaagtgct    540

actgacacgg gagctggaaa cgatagaaga acgctaagga gaaggaatgc ttctaaagac    600

acgagaggta acaacaacaa tcaagatgaa tctgattttc aaactggtaa tggttctgga    660

agtaatggcc atggttctag acaagggtcg caattccccc atttcaacaa cctaacctac    720

aagtcaggca tgaactctga ctcagatttt ctacaaggta aaatgaagg tactgatcta    780

tatgcatttt tgtttggcga aaagaacccc aaagacaatg ctaatgggaa tgaaaagaaa    840

aaaaccgtg gtgctcaacg atattccacc aaaacagctc caccttaca gtctttgaaa    900

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cctttcagac taaggtctga ctaa    984

<210>    133
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<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    133

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attcgtcagg gatccttgaa tggtcccaga ttaattacgt gtggacatgc catttcccaa  180

actggtggtc atggcgatct gagatctggt gccctacctg ctagtgcctt tgacagctgt  240

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gccagagaag agtttagaag aggtgcagac tttattaaga ttatgggtgg tggaggtgtg  360

gcctctccaa ctgacaaaat atcaaacaaa caattttgcg acgacgaaat aaaagcactt  420

gtagatgtcg caaatagtta ccacacatac gtaacagcac acgcctacac tgcggaagcg  480

atacaaaatt gtatcaagtt aggtgttaag ggtatcgaac acggaaactt attagatgaa  540

cgtaccgcag agcttatggc agaattgggt tgctacttga ctccaacact agttacctac  600

aaagtgatgg gttctgatca atttagtgca ttcttgggac ctgaaaatag tagaaaaaat  660

acagaggtgc tttacaaagg aattgatgca atgaaaattg cccagaaaaa aaaagttaaa  720

atttgttttg gttcagattt attgggtcct ctatatggtt atcaaacgca agagtttcgt  780

attagaggga aagttcaaac gacacaagag attttgctct cagcaactgt tactcctgcc  840

gaaatgaacg gattaggcga taaattggga cagattaagc cagggttcat tgctgaccta  900

ctgatgatga aatcaaatcc gttggacgat ataacgattt ggatgaacc cgagagcaac  960

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&lt;210&gt;      134
&lt;211&gt;      1215
&lt;212&gt;      DNA
&lt;213&gt;      Saccharomyces cerevisiae

&lt;400&gt;      134

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tttgagagcc agatgtcgtg gctaaggttt caaacaaggc agtatctaac tagattcaca  180

gacaaccaat cagatttcgt acattcttta caaaaaaagc acagaacgcc ttttagagac  240

gtttatttca aatacacttc gcttatgggt tcccacatgt tttatgttat cgtgcttccc  300

atgcctgtgt ggcttggata ccgcgattta acacgggaca tgatctacgt tcttggttat  360

141

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cattctgcta acgctactgc ggtaagtcta ttattctttt ggagaatatg tttatctgac  540

acactggtat ggccaacaaa gcttctttta ctgagtctgg tgatattta ctacttaacc  600

ctggtttttg gtagagttta ctgcggtatg catggtatgc tggatttatt tagcggcgcc  660

gcagttggag ctatctgttt ttttataaga atctgggtgg tgcatgcttt acgaaatttc  720

cagattggtg aacatctctg gtttcccctt ttgagtgtag catggggctt gtttattctg  780

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gtatgtagta ggtacgcatc atgtggttct aaggtgttct tgaggcctct ggtaggtgtc  960

gcttctgtga ttgtttggaa agacgtcatt agcaagacag ctgtctacac gctgttaatt 1020

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gaagaagaag agtgtttatt gtacagcggt gtttccaaag tggaaatcgt cggaaggttt 1140

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<210>      135
<211>      429
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      135

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atccatttct taggcagccg agacacgaac ggtcccagtc catccaatct ttcctttctt  240

gcaacttcca actctttcga cgtaaacaca ggtgctgatt ctttcgagga aggggaggag  300

gaggaggagg aagaagacgt atatctcttt ctgctgcttc caatgattcc agcaacggta  360

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142

<210> 136
<211> 1548
<212> DNA
<213> Saccharomyces cerevisiae

<400> 136

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actggtgaca atgtaggtgg cgccctgaga gttcccggtg ctatctccga gaaacagtta   180

gaagaacttt taaatcaatt gaacggtact tcagacgatc cagtgccata ccttcagc    240

tgtacaattc aaggtaagaa ggccagtgac cctgtgaaga cgattgatat aacagataac   300

ctatattctt cattaataaa accaggctat aacagtacag aagatcagat cacgctactg   360

tatacgccaa gagcagtttt caaagtcaag ccggtaacta gaagttcatc agccattgca   420

ggtcacggtt ccacaatttt gtgttctgcc ttcgcaccac atacgagttc taggatggta   480

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cactgggtta atcacttatc tttatctaca gattacgcat gcgcattgg tgcattcgat  1020

catacaggta agaagccttc tacaccagaa gaagcccaga aaaaggcatt ggaaaattat  1080

gaaaaaatct gtaaaaagaa tggaaattca gaagaaatga tggttactgc aagcgatgat  1140

tataccatgt ttttatggaa cccactaaaa tctaccaagc ctatagcaag aatgaccggt  1200

caccaaaaat tagtcaatca tgtggcgttc agccctgatg gtaggtatat tgtctcagcg  1260

tcttttgata actctatcaa actttgggac ggtagagatg taagtttat ctccacattt  1320

agagggcata tagccagcgt ataccaggtt gcgtggtcat cggactgccg actactggtg  1380
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143

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gacctccctg gtcataaaga cgaagtttat accgtcgact ggagtgtcga cggtaaaaga 1500

gtgtgtagtg gtgggaaaga caagatggta agattgtgga cgcattga          1548


<210>     137
<211>     1731
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     137

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ccttccttga taaaactaca ctctgaattg aaattggatg agctgcaaac tgataacacc  180

cctgattacg tccgtttagt tttaaggtcc tctgtatacg atgttattaa tgaatctcca  240

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ccatctatta agtatcaaaa tgtctcgaga ttagggtctc aagtcgtcct atatggtaac  540

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ggtttaattg ctggtattgg tgcttatttg aaaagggttg ctcctcatat caaaatcatt  780

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144

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tccgttcctc caagggaaaa cttaaccttc caaaaattct tggaagattt aggctacact 1680

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<210>      138
<211>      3570
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      138

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gcgcaaagcg ccggagatgc ctctttgcag tatgctaatc tgagatctgc caatgtgagt  180

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aatgagatag atctggacga ttccgcacca gtgtcacttt ataagtcggt aaaacgatcc  480

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cgtagtgcca ctaatggatc catgagggtt tctaccccat ggctaggca aatttatcct  660

ccaccttctt cgaagatcgt ctccaacaac tcagatgacg aagacgaaga cattggtgaa  720

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145

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cataaaaacg aattggtttt ctctgcttca gcttcttcct cttcatttgc taatggtggc 1020

acagctgctg tcactgctca ggacattaat aggaaaccac ccgtaaccac tccaagaata 1080

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gctaagaggg ctgcccaatt attggcaggt gccaagaaaa acgaagtccc acagaaaagt 2100

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gatttctcat cagacgatga tttttaaaagg aaaaatatgt cggtgcctaa taatgggccc 2220

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atcaataaag aagttgatga agaaagaaac gacaaaagag atagtcaaaa aaagtcagcc 2340

gtgagtgaat cttcagtaac aaatagcaaa ataagtgaac aaatggcgaa aagctttat 2400

ccgaattcaa acaagaagca aaatgaagct acaaaggtgg aaactaagcc agcaacacaa 2460
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146

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ggaggtgaag acttgaacaa gaaagcagag gggtccaagg aaccagaaaa agcatctgcc 2700

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ccttctttga gttcattatc tgatcttgtt tcaagaggca tcccagatgt aaaggaaaaa 3300

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agtgcgaaat ccgctagtgc tgctttaggt aagaagaaga agccaagtgg tggatttgca 3540

tcattaataa aagatttcaa gaaaaaatga                                      3570

<210>      139
<211>      2082
<212>      DNA
<213>      Saccharomyces cerevisiae

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147

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148

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149

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152

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154

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<213>      Saccharomyces cerevisiae

<400>      144

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<213>      Saccharomyces cerevisiae

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156

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      146
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ttctatcacg ggtcagatga cttgatatgg gggaagttct ttgtctgcgt gtacaagtcc   240

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157

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158

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<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    147

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actaccatga agtacgtcga acctggtaat gctatgtccg gcgaaggtga gaagctgcaa   240

gttactaccg tcagagacta cgatttgaag gaaatagaca gtgctatcaa gtctatctac   300

actggtatgg ctatgatggg tttcatgcat ttgtacttga aatacaccaa cccattgttc   360

atgcaatcca tttctccagt gaaaagcgct ttggaacaca cgaagtgaa aattcacctc   420

ttcggtaagc ctgcaaccgg cgatttgaag agaccattca aggctccatc tttgtttggt   480

ggtatgggtc aaactggtcc aaagaccgac aagaaatcta tcgaagaagc tgaaagagcc   540

ggtaacgctg gtgttaaggc tgaatga                                       567


<210>      148
<211>      435
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      148

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cagtccttca cggaaaaaaa aaaagagcac tgggtcactt cggaaaaact tttgactcaa   180

tgcaacagtg tcataatcct ttgcgctgtc tctttgaaga aaaatcagga gtgcaagata   240

tcgattaatt ccttggaagt tatgatggtt agtcttagtt taactctctt gaagaagggt   300

tttttcagtt ggtcaacact ctttagaggt aaaaaaaaaa aaaaaaaaaa aaaaaagaga   360

attcttcatg taatttacca tgattctacg tttttgcaag caaaaatgaa gataatccga   420

gcgcatgcga agtag                                                    435


<210>      149
<211>      351
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      149

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gaggaaaatt cgatatatct ggtatcactt tattattcct tcagcacgaa atgtcgagcg   120

atctcgatgc aggaaccagg tataagtagc gatagtaaat tttttctct cttttaata   180


160

atccggaaag tctcagttgc gagtgattgc agacagttgt atgaatgtaa aaaaagtaat  240

gaaacattt gggagtattt caaacggagg ttagagacga ggctttcgag cttttctatt  300

attttaagtg ctgtgtttcc ggacgtgctc ttcactttct tattttcttg a  351


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<211>    642
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    150

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atatggattt tgtttgtgct gtttgttgcc gcagtaatcc ttataatact gttcactttt  180

gtagcgaaca gaaggagacg aaggatgggg cgtgctccca ttagaggtac ggcatggttg  240

acaccgcctt catacagaca gtctcagcaa caatatactg ggaccgttca gcaacggaca  300

gatgattatg ttcctgagta tacagaaaca gcgaacgaac atgatcttgg atactatgac  360

cagcggggcg agtttcaccc caacgataag gctgcatacg tggcccccccc gccattggta  420

caagaatgtt catcagaatc tgttaattct ttagaaagac ctcccgctgc tgtagttcac  480

caagctaact ctttagatac ggattacggt ttaacaaggc ctagcaatgg gcgcgttcca  540

gctgtaagtg atacggtgga gcaattggaa aggcttccgg gcgggactac aacgcaggaa  600

attaacccac cggagagggc aaaggtaaat gcaaggtcat ga  642


<210>    151
<211>    3042
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    151

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aaatgtaggc tatttcacta caataaagtt catggactta gcctttctag tgaagggaaa  180

attttggcct atggtgcaag atcagtaaca atagtggaac ttgaagacgt tttaaagaaa  240

gagtcattgg tggatttcga aaggattaac tcagattgga ttaccggtgc tacattcagc  300


161

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tttgacaact tgcaaatata tttgttaaca tgttataata aagtgctaat ttgtgattta  360

aattgtgaag ttctttttag gaagtctctt gggggagaaa gatctattct atattccggt  420

ataattaaag ttttcggtcc ggataaagta tatgttaacg ctggtactgt aatgggcggt  480

gttatcattt gggacctgtt ctcggagaca aaaattcata acttactggg tcatgaaggt  540

tctatctttt atgttaattt aagcaacaac ggaagatatg ttgccagttg ctctgacgac  600

agatcaatta gactgtggga tttagaaact ggcaagcagc tgtctgttgg ctggagccat  660

acggcaagaa tatggaattt aatgtttttt gataatgatt caaaactaat aagtgtttct  720

gaagattgca catgccgtgt atggaacatt atcgaatcac gagaaaacgt tgccgaatta  780

tccatatcta acgtttacga agtacattta atcaagagta tatggggcgt tgatgtgaaa  840

gacgacgaaa tgatagctgt aacctccggg aatgatggta ggttaaagct gattgatctt  900

cttcaactga agagacacgg cgatgaagaa acatcgttca gtctagatga tatcgcaaag  960

caatgtggcg atattttcga aaagaatgaa agtatcaagg gatttcaatg gttttcattc 1020

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acgcaaaata tcgctgtctt ttccaataat aaaagtgaca tccttcttat caaatttagc 1200

aaagatagcg ctgacataat tgagaccgaa gaattccatt tagatgagct ttctaagaca 1260

aataactgtc tcgttacaga atacgatgat gactccttcc tattgacttt acaatcccca 1320

aatcctcgag agaagtttgt atgtttggaa ataagccttc agaacttaaa aattaaaagc 1380

aagcactgtt tcaataagcc ggaaaatttt tcttcctcat gtttgacctc cttccgaaat 1440

catattttag tcggctcacg ttttagtaca ttagtaatct acaacttact tgatgagagc 1500

gaggagccct tcataattag gagattaagt cccggagaca ctacaacctc aatcgaattt 1560

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tttattgagt tgacgaaaaa cagtttggaa gagggtccct accgactaag ttataaggtc 1680

ttgcattcta ataagatgat gaaaggtttc ttggagggcg ctttctttaa ttcaaaaggt 1740

gaatacatta cttatgggtt caagtccagc ttgtttttatc tctacaatga aaccaactgt 1800

tatgaactag ctagtgaagt ttgtggtggt tcccatcgtc tgtggaatct cgcaaaaatt 1860

actgatggcc acgtattaat gtatattaag gcatcccgat ttcatttaag gaaaatttac 1920
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162

aactccattg tgcctgaaac tttagaaaat ggtgtacacg gaagggaaat cagagatatt 1980

tcaatctgtc ctgtttcaaa taccaacacg aatgacaatt ttaaggatgg gcatatattc 2040

tgtactgcat ctgaagatac tacaattaag ctgggatatt ttaacaatag aacagggaag 2100

gtgcagaatt tttggacaca aagaaagcat gtgtctggat tacaacgttg tcagtttata 2160

aatcacaaac taatgatatc atcttcagct agagaggagt tattcttatg ggaattgaac 2220

gataagtata ataaacgacc atatatgacc atacgacaag ctttacctgt atccacaaat 2280

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tccggtatgt tgattaatgg tggcaaagaa gtcattacca catcggttga tcaagtaata 2880

cgcgcttggg aaattaccgc aggcaagctt tcactggtag ataaaaagcg taccactgtg 2940

gcggatacag gatcattaga aatcatttcc aatgatgaag atgctgattc tgagaaaacg 3000

ttactgatcg gaggtgttgg tttatcaatt tggaaaaaat ga                3042


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<211>      933
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      152

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gactacgctt ccaccttcgg tattgccgtt caaccaatct ccactacatc cagcgcatca   180

tctgcagcca ccacagcctc atctaaggcc aagagagctg cttcccaaat tggtgatggt   240

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caagtccaag  ctgctaccac  tactgcttct  gtctctacca  agagtaccgc  tgccgccgtt  300

tctcagatcg  gtgatggtca  aatccaagct  actactaaga  ctaccgctgc  tgctgtctct  360

cgtgatggtc  aaattcaagc  taccaccaag  actacctctg  ctaagactac  cgccgctgcc  420

gtttctcaaa  tcagtgatgg  tcaaatccaa  gctaccacca  ctactttagc  cccaaagagc  480

accgctgctg  ccgtttctca  aatcggtgat  ggtcaagttc  aagctactac  taagactacc  540

gctgctgctg  tctctcaaat  tggtgatggt  caagttcaag  ctaccaccaa  gactactgct  600

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gctgtctctc  aaatcggtga  tggtcaagtt  caagcaacta  ccaaaaccac  tgccgcagct  720

gtttcccaaa  ttactgacgg  tcaagttcaa  gccactacaa  aaccactca  agcagccagc  780

caagtaagcg  atggccaagt  ccaagctact  actgcttggc  tattggtgac  aatgatgtct  840

tctaccaatg  tttgtccggt  actttctaca  acttgtacga  cgaacacatt  ggtagtcaat  900

gtactccagt  ccacttggaa  gctatcgatt  tga                               933


<210>        153
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<213>        Saccharomyces cerevisiae

<400>        153

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gtcttggtca  gaatctcgat  tatccttcac  catgacgaga  atgcgtatac  gcagagccaa  180

tataatctgt  atacgggacc  tttgacatta  aggtttctgc  agagagttta  ttacatgcat  240

tttcatatat  atattttaa  cgccattcct  ttacggtatg  taaagaaaaa  tgatccaatg  300

agcggcccgtt  cgtacgagat  gagatataat  aagaatgaaa  gatag              345


<210>        154
<211>        375
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        154

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164

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tccgcgttct ctcttttcg ctcttttctg gctaccgcgc ccgccttata tataaaatct   120

cttccgaata acaaagtggc cgaaacaagc gccaacgtcg accattttgc caccgtgtca   180

ctgtgcacga gcaacgaaaa actggcgttg gttgcgcctc acgaattgct tgagcctctt   240

cccaatatca tcgcgcattt atttgagtca ttctctgccg ctttattatt aaaagtctgt   300

gtgctatcaa aatgctcttg ctcctgttca ccctctatgc gtaaacactt gcgcgtttct   360

cccttctct tttag                                                     375
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<210>     155
<211>     1644
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     155

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ggttccggcc attcttctga cttagcaaag tcattagaag actatcggcc tcctgatgaa   180

aagccgtcct cattgtcatc tgtgggggaa ggtggcgcta atgaggaaga gaagggcggt   240

aacgacggcg gtcccttggc aagaattcaa acagggcttt tttctccaag actgcgaaat   300

cataggaaaa agattctctc gaagtttgtt ttgaacaact tcttcattgc ttgtgtgtgt   360

gtatcgctca tatcgattta ctggggtgcc tgttacggaa cagatcgtta cttttttcaaa  420

gtgaaaaata ttgttgtatt gcaggatgcg ccatctaata cttcagttca atctatttcc   480

gcgatcatac cctcattgtt agcgtctgtc cccgggacat ggcatatata caacgcaaca   540

tcatttcata ggaaatttgg tacgacgaac tccaccgaaa ttgacagaaa gatagtcgat   600

ttaatttacg atgagagata ctggctggcg ttaaacgtta aacctaatgc tacagacact   660

ttgtataatt ctttgattag ccaagacgca aactcggagt tcaattcatc aattttttttt  720

gaatccgtgt ttgaaagtgg tcgtgaccca tcgagtgtta aatcgaccat tctaccactc   780

atgcaacaat ggaggtccg ccttcagaaa tattacgtca aggaatatct tccctcattg   840

atgagcaaca tcacttctaa tgacagagat cttaatataa acatggagaa ctgggcgatt   900

gcaggacagt tgttgttcac ctacaacgat tatcgtccct tgctgatcg tattctaatg   960

gccctctgc aggtcggtct gatttattgt attttgttaa ccgttttaca actgtcatta  1020
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                                165
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aggcttctaa tttcctgggc aacttatttt cttctttcca ttggattctg taccgtatct 1140

gcaattttta ggatcgattt cacccccgcc tttggcagag gaggattcgt agtatattgg 1200

atgtctacgt ggttggtaat gatggctgtt ggtggtgcca atgaaaacgt tctcagctta 1260

gttatagctt actgccctcc atacctgagt atttggttga tgacgtggat catattaaat 1320

atttctgctt cattctaccc aatggttttg aacaacgaat tttacaggta cggctacata 1380

atgccaatcc ataatgccgt ggatatctat aaagtgattt ttttgaattt aaccaaaaga 1440

aaaatgggaa gaaattacgg tattctcgtg gcatgggttg ccctcaatac atccttgatg 1500

ccattttgta tgaagtttgc aggtaaaaaa atgcaaaaaa atgctatgca agcagcagaa 1560

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                                                                   1644
ataacaacc cgcccggaaa ttaa
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<210>    156
<211>    1761
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    156

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gtagatttca ccggtgaagg tgccaaatac acaactgcta cggagggcaa tggtggtgca  180

gatttagcga ttcaaagaac gacgactatg aattctgctg cagaatcaga ggttaatatc  240

acgagaagat taactaaaat ccttactggg tctgttaacg agcctgaccg tgtagaggtt  300

gattatacca attgtgcgcc catgggtggt gacagacctt accctccatc gttgccgagc  360

agagacctgt acgaggttac ttttgatggt cctaacgacc cactacatcc atttaactgg  420

cccatgaaga agaaagtgct gctatgtctg gtcttatgtc tggattctat tgccattgct  480

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atctatgctc ctctttctga attgtacggt agaaagggtg ttctggtttt atctgcgttt  660

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166
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ctatggagaa gagatgaaca cggtactgtt ctctgtaatg catgtggcct cttcctgaag   180

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aaaatattca agagaaagaa gagactgctt acaactggtg gtggttcatt acctacgaat    360

aatccgaagg tttctattct ggaaaagttt atggtgagcg ggtccattaa gccactgtta    420

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ccttttttcag attccgctgt accagaaata gaactaactt ggaagctaca taatgaggag    660

gaggtaatca aattgaagac caagataagc gaattggagt tggtgacaga cctatacaaa    720

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gacccttttt tcaaaatgct aaataaatct ctagctaatt tcatgaacgc tatgacaggt    360

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ggtgtttatt tagactccac cttgaatccg ctacttaaac aagaagattt tgatcaggag    480

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aaaacttttca cgtacggtaa cttgccattg gtggatacgt aaagcaatt aaatgagcag    780

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169

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<212> DNA
<213> Saccharomyces cerevisiae

<400> 159

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ttcaagcaaa gtaacctgca tgtcattcca gaagaccttg aaaacagcga acagacagag 180

caggaaaaaa tccaatggaa actagcttct cagccctatc aaaaagtctt gagccaaagg 240

cacttgacca tgattgccat aggtggtact ttggggacgg gactgttcat tggtttaggt 300

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tatgccacac atgtcagtag gttcatagat gaatcggttg gctttactgt ggctacaaac 480

tatgctttgg cttggctgat ttcttttcca agcgaattaa ttggttgtgc acttactatt 540

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gggcctaact ctactggtta tattggcgcc aaatactggc acgacccagg tgccttcgca 780

aaacctgtct tcaagaattt gtgtaacaca ttcgtttctg ctgctttttc ctttggtggt 840


170

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<212>      DNA
<213>      Saccharomyces cerevisiae

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caggaattga gcaacaacaa gcaagaaaga agcagttctg taacttcggc aagctctcat    180

tatattggct acctcagga ggcgcaaatt aacggtgaac ccttacaaag ggccaatgtg    240

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ttcctggaag agctgactgc caatgccact catgcagcaa actctggtat tccgccagct    360

aataacccag tttcttctgg ctcaactgcc cagcggcctt cagtcgagga attctttttct    420

171

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tcatttgatt cacatccacc cagggtcaga agctcatcca agagtgctgt aatcactccc  600

gtctctaaaa gcgttccaga tgtcgatcct gctgttgtag atgtcgcaaa agttagagaa  660

gagtttcaac agcaagcctc cttgccttcc atgaaaagag tttccggaag caccgctgga  720

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gaatacatcg aaaaagttgt tttgatccaa atctgcatcg gtaagagttc cgatcctgag  1860

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172

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gaatacataa ataatgcttg ggagtccaac caagaaacgt ctactgtttt caatttggct 2340

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<212>      DNA
<213>      Saccharomyces cerevisiae

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cagtacataa aagcacgtat gaaagataag accttcttct atacgaagca attccgtaca   180

gccaaaaaca aatttttctt tcatctgtac cattgggagg ccactcatat taacgttgac   240
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173

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tccgcctga    309


<210>    162
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<212>    DNA
<213>    Saccharomyces cerevisiae

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aggttcgctt ccggacgagg atttaagagt cttgtcaagt ccaaaccttt cctgcactgt    540

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174

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aaaataaaag aacaaataaa ggcttctgat actataccga aaatagccag ggtcgttgcc 2760

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175

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<211> 1023
<212> DNA
<213> Saccharomyces cerevisiae

<400> 163

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attttcttgg ctcaaaccaa aggttacttc aaggagcaag gtctagacat ggccatccta   120

gaaccaacca atccttccga tgtcactgag ttaattggat ctggtaaggt cgacatgggt   180

ttgaaagcca tgattcacac cttggctgcc aaggcccgtg gtttcccagt gacctctgtt   240

gcctctttgt tggacgaacc atttaccggt gtcttgtact aaagggcag tggtatcact   300

gaagacttcc agtccctaaa gggtaagaag atcggttacg ttggtgaatt cggtaagatc   360

caaatcgatg aattgaccaa gcactacggt atgaagccag aagactacac cgcagtcaga   420

tgtggtatga atgtcgccaa gtacatcatc gaaggtaaga ttgatgctgg tattggtatc   480

gaatgtatgc aacaagtcga attggaagag tacttggcta agcaaggcag accagcttct   540

gatgctaaga tgttgagaat tgacaagttg gcttgcttgg gttgctgttg cttctgtacc   600

gttctttaca tctgcaacga tgaattttg aagaagaacc ctgaaaaggt cagaaagttc   660

ttgaaagcca tcaagaaggc aaccgactac gttctagccg accctgtgaa ggcttggaaa   720

gaatacatcg acttcaagcc tcgattgaac aacgatctat cttacaagca ataccaaaga   780

tgttacgctt acttctcttc atctttgtac aatgttcacc gtgactggaa gaaggttacc   840

ggttacggta agagattagc catcttgcca ccagactatg tctcgaacta cactaatgaa   900

tacttgtcct ggccagaacc agaagaggtt tctgatcctt ggaagctca aagattgatg   960

gctattcatc aagaaaaatg cagacaggaa ggtactttca gagattggc tcttccagct  1020

taa                                                                 1023


<210> 164
<211> 2781
<212> DNA
<213> Saccharomyces cerevisiae

<400> 164

atggagcaga atattattag taccataagc gatgagtgta ttcgtcaccg gtcgaagtac    60


176

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cttacgatag cacaactaac cgctattgca gaggctaaaa ttaacgaatt catcataact  120

ggtaaggcaa aagatcaaga tttgagcagt cttctagata aatgcatcga tattttatct  180

atttacaaga agaactcgaa agatatcaaa aatattatat cgtgcaaaaa taagggtgca  240

atgattagtt caaattccgt aatgattatt caattaaatt atgtttacta caaggtaatt  300

cacattattg taacaaccaa tattcctcat ttaagtgaat tcgccaagat taaattacat  360

aagagcacga gtgatgaggg caacggtaat aacaacaata atgaatttca actcatgaac  420

atttacaaca ctttgctgga aaccttatta aaagatgaaa acattgcaaa aataaaaagt  480

ttcattaagt cttccataaa acaaacaaaa ttgaaccatg agcaagaaga atgtaacctg  540

atgagaacgg gttcctatat cacttccaat caattaaact ccctaataag ttcatcagca  600

aattctgctt cctcccaaat ggagatacta ctgatagata tacgatcaag gttggaattc  660

aacaagtcac atattgatac aaaaaatatt atatgcctgg agcctatttc ttttaaaatg  720

tcatattcag atcatgattt ggagaaaaaa tcattaatta cttctcctaa tagtgagatt  780

aaaatgtttc aaagtagaaa tcttttcaag tttatcattc tctatacaga cgcaaacgaa  840

tacaatgtta aacagcagtc tgtcctgttg gacattctgg tgaatcattc ctttgaaaaa  900

ccaatatccg atgactttac caaaattttc attctggaat ctggttttcc aggttggctt  960

aagtcaaatt atgggaggca agtatcatca tcttttccat caaataacaa tattaaagat 1020

gatagtgttt atattaatgg taacacttct ggcctaagtt tacaacattt acctaagatg 1080

tctcccagta taagacattc aatggacgac tctatgaaag aaatgctagt tgcgcctact 1140

ccattaaatc atcttcaaca acagcaacaa cagcaatcag acaatgatca tgtgctaaaa 1200

agatcttcaa gtttcaaaaa attattctca aattatacgt ctcctaatcc gaagaattca 1260

aattcaaact tatattctat atcttcgttg tccatatcta gttcaccatc gcctttacct 1320

ctacattcgc ctgacccagt taagggcaat tcattgccaa tcaattatcc ggaaacgcca 1380

catctttgga aaaacagtga gacagatttt atgacaaatc aaagagaaca gttgaatcac 1440

aactcttttg ctcacatagc tcctatcaac acgaaggcca tcacttctcc atcaagaact 1500

gccacaccga agttacaacg cttcccgcaa acaattagta tgaaccttaa tatgaactcc 1560

aatggacaca gttctgccac ctctaccatt caaccttcgt gtctatcctt gtctaataat 1620

gactctttag atcatacaga tgttacacca acttcttctc ataattatga ccttgatttc 1680
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177

gcggttggtt tggaaaatct aggaaattcg tgttacatga actgtatcat tcagtgtatc 1740

ttaggtacac acgaattaac ccaaatcttt ttggacgatt catatgctaa acacatcaat 1800

attaatagta agttgggatc gaaaggtatt ctggcaaaat attttgcaag gttggttcat 1860

atgatgtata aggaacaggt tgatggttca aagaaaattt ccatatcacc gataaaattt 1920

aaattggcat gtggatctgt taactcatta tttaagactg catcccaaca ggactgccaa 1980

gagtttttgcc aattccttct agatggtctt catgaagact tgaaccaatg cggttcaaac 2040

ccacctttga aggagctttc tcaagaagct gaggcgagaa gagaaaaact gtctttgcga 2100

attgcctcgt caattgagtg ggaacgattc ttgactactg atttcagtgt tattgtcgac 2160

ttatttcagg gacaatacgc ctcacgacta aaatgtaaag tctgtagtca tacctcgaca 2220

acataccaac cttttacggt gctgtcaatc cctattccta aaaaaaattc ccgaaataat 2280

attaccattg aagattgttt cagagagttc accaaatgtg agaacttgga agtggatgag 2340

caatggttgt gcccacattg tgaaaaaagg cagccctcca cgaaacaatt gacaataacg 2400

agattaccga ggaatctgat agtccattta aagagatttg ataatttatt aaacaaaaat 2460

aatgacttcg tcatataccc tttttgttg gacttgactc cattttgggc caatgatttt 2520

gacggggttt ttcctccagg tgttaatgac gatgaactac caataagggg acaaatacca 2580

ccttttaagt atgaattata tggtgtagca tgccactttg gtactttgta tggtggtcat 2640

tatacagcct atgtgaaaaa gggattaaag aagggatggc tatattttga tgataccaaa 2700

tataaacctg tcaaaaacaa agccgatgca attaactcta atgcatacgt tttgttttat 2760

caccgcgtct acggtgtttg a                                         2781


<210>        165
<211>        1464
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        165

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tacatcaccc tatcctacac tccaaattca ggttttttcct tggaccaaat gccagctggt    180

attatggata ttgctgcgca attggttgca aatccaagtg atgactccta caccactttg    240


178

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tactctgaag tggacttttc tgctgttgag catatgttga ctatggtccc atggtactct   300

tctagactgc ttccagaatt agaagcaatg gatgcttctc taactacctc aagttctgct   360

gccacatctt caagtgaagt tgctagctct tctattgctt catccactag ctcttctgtt   420

gcaccatcct caagtgaagt tgtcagctct tccgttgcac catcctcaag tgaagttgtc   480

agctcttccg ttgcaccatc ctcaagtgaa gttgtcagct cttccgttgc ttcatcctca   540

agtgaagttg ccagctcctc tgttgcgcca tcctcaagtg aagttgtcag ctcttccgtt   600

gcttcatcct caagtgaagt tgccagctcc tctgttgcgc catcctcaag tgaagttgtc   660

agctcttccg ttgcaccatc ctcaagtgaa gttgtcagct cttccgttgc ttcatcctca   720

agtgaagttg ccagctcctc tgttgcgcca tcctcaagtg aagttgtcag ctcttccgtt   780

gcttcttcta caagcgaagc tactagttct tctgctgtca catcttcctc cgctgtttcc   840

tcttcgaccg agtctgttag ctcttcctct gtcagttctt cctcagccgt ttcctcttct   900

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agcgttatta tctcaaccag aaacggtacc actgttactg aaactgacaa cactcttgtc  1140

accaaagaaa ccactgtctg tgactactct caacatctg ccgttccagc ttccaccacc  1200

ggttacaaca attctactaa ggtttcaacc gctactatct gcagtacatg caaagaaggt  1260

acctctactg caactgactt ctctacacta aagactacag ttaccgtatg tgactccgcc  1320

tgtcaagcta agaagtctgc taccgttgtt agcgttcaat ctaaaactac cggtatcgtt  1380

gaacaaaccg aaaacggtgc tgccaaggct gttatcggta tgggtgccgg tgctttagct  1440

gctgttgccg ccatgctact atga                                          1464


<210>      166
<211>      534
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      166

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gttccggtac ttctaacaat caataataat gtggtccata ttgcgcaagt taaaggtacc   120
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179

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tctatgcagc ctacgctgaa cccgcaaacg gaaacgctgg caacagattg ggtgctgctt   180

tggaagtttg gagtcaagaa cccaagtaat ttatctagag atgacattat ccttttcaaa   240

gctcctacaa accctcggaa agtttactgc aaaagggtta aaggtttacc gtttgatacc   300

attgacacga agtttccata ccctaaacct caagtgaacc tgcccagggg acacatatgg   360

gtcgaagggg acaattattt tcattcgatt gatagcaata cttttggccc catttccagt   420

gggttggtca tagggaaagc tataacaatt gtttggccac cctccaggtg gggaacggat   480

ctcaaactga gtaccggtag agactgcatt agcaaaagag ccattttaga atga         534


<210>      167
<211>      1395
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      167

atgggacaaa ttctatcaaa cccggtaatt gataaagaga gccactccgg tgctgactcc    60

ttgaccgcgt ttggactgtg tgcaatgcaa gggtggcgga tgtcaatgga ggattcacac   120

attctagagc ctaatgtttt gacaaagtcc gataaggacc atattgcatt ttacggtata   180

ttcgatggtc atggtggcgc taaagtagca gaatactgtg gtaataaaat agtggagatc   240

ctgcaagagc agaaatcgtt ccatgaagga aatttaccaa gggctttgat tgatactttc   300

ataaacacag acgtgaaact gttacaagat cctgtgatga agaagacca tagcggatgt   360

acggctacat ccatattagt atcaaagtcc cagaacttgt tagtatgtgg taacgctggt   420

gacagtagaa ccgtactcgc caccgacggg aacgcaaagg cattatcata cgatcacaag   480

cccactctag caagcgaaaa atcacgtatt gtggcagctg atggcttcgt agaaatggat   540

agggtcaacg gtaacttggc gctctctcgt gccattggtg attttgagtt caaatccaac   600

cccaaattgg gccccgagga gcaaatagtg acatgtgttc cggacattct cgagcattct   660

ctagattacg atagggacga gtttgtaatc ttagcctgtg atggtatctg ggattgtttg   720

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gaaatttctt cgcggatcat cgatgtctgt tgtgctccca ccacagaggg gacgggtatt   840

ggatgcgaca acatgagtat agtggttgtc gcgctgctga agaaggtga gacgtcgct   900

caatggagcg accgtatgaa gtccaaggcc caccgcacat cagtgcgttc ttttgcagac   960
```

180

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aagagaagaa gggtgtttag ttactacgat ttttccaaat gtaacgacga acaggtgttc 1020

gctatcacta cgaagaaacc tcaggacaaa ttcactcgcg accacgaagc cgctgtggcc 1080

tcggtgactg ccgccgataa cgacgatcca atggacatag acgacacgga cgctgacaca 1140

gatgcagaaa atcttgaccc ttccagccaa tccaagagca agacctccgg ccccattgat 1200

ctagcatcct tggaggcgct acttggtgct acaggaggag tgaagacaga cagcaacggg 1260

aacaaagtca cctacactct tccccagtct gccttggccc aactgctcca aaccatgggc 1320

catgacccgg cttcctccca tcccgagaat gacagtaaca ctgaccacaa ggccggccgt 1380

tcccacttgc aatga                                                  1395
```

<210>      168
<211>      363
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      168

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aggcatctta cacgcactgg atggtctctt aagtgcttgt gtagctggtc cttgttggtg  120

ccctcaggct cctcccattg cgagtgcttc gtctctggat tgaaaaaata ctctcttttc  180

ttggacttac tatacctgac ggtccacggg gttggcagcc cggtcctcga tgctacgtca  240

gatggcattg gtgcgtcgtt gtggtgccgt agtcggttat gcgtgggaat aagtaccaca  300

atgatcattc aggtcctttt tctacttaga tcgaagggaa aaaggtatga tacccgctcg  360

tga                                                                363
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<210>      169
<211>      1845
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      169

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atcgccttat taccagttat ttccatgcta tgcgctctat ttgggtttat ttctatagct  120

attctgccta tggatggaca gtacagaaga acatacattt ctgagaatgc attgatgcct  180

tcacaagcgt atagttactt tagagaatct gaatggaaca ttttgagggg ctatcgatct  240
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caaattaaag aaatggtaaa catgacttct atggaaagaa acaatttgat gggttcttgg  300

ttacaagaat ttggtactaa gactgctatt tacgaaaatg aacaatatgg agaaacattg  360

tacggtgtaa tgcacgctcc tagggggtgat ggaacagaag cgatggtgct tgccgttcca  420

tggtttaatt cagatgatga attcaatatt ggcggcgcag ctttgggtgt atctttagca  480

agattttct cacgttggcc agtatggtcc aagaatataa ttgttgtctt cagcgaaaat  540

cctcgtgcag cattaagatc atgggttgag gcataccata cttccttaga tttgactggt  600

ggttccattg aagctgctgt tgtgttggat tattcgagta cggaagattt cttcgagtat  660

gtagaaatct catacgacgg tctgaatggt gagctgccca atttggatct tgtcaacatc  720

gctatatcca ttacggaaca tgaaggtatg aaagtttctt tgcacggtct acccagtgat  780

cagttaacta ataataattt ctggtcaaga ttaaaaatat tatgcctggg aataagggat  840

tgggcgttgt ccggtgttaa aaagccccat ggtaacgagg catttagcgg ctggaggatt  900

caatctgtaa cattgaaagc acatggaaac agtggtcatg atattactac atttggacgt  960

atacccgaag caatgtttcg ctctattaat aaccttttgg aaaaatttca ccaatcgttc 1020

ttcttttatt tgttattagc accacgtcag ttcgtatcca ttagtagtta tttgccaagc 1080

gctgtggctt tatctatagc attcgccata agttcattaa atgcatttat aaacaatgct 1140

tatgcaaata tatccttatt ttccgagtat aatttggtag cgttgttggt ttggttcgtg 1200

tcattggtga tatcatttgt tgtttcacaa gcgtttcttc taataccttc atcgggatta 1260

ttgatgacaa ttagcatggc atcttgtttt ttacctttga tactttccag aaaaattcac 1320

atctcagaac cactatcata caggttgaaa aatgttgctt ttttatattt cagtttggtt 1380

tcaacatctt tgctaatgat aaactttgca atggctttac tgatcggcac attggcattt 1440

cctatgacat ttgtgaagac cattgttgaa agttctagcg aacatgaggt gacaactcaa 1500

tcctctaacc caataaaaac tgagccgaaa gatgagatag agctcgtcga gaatcacatg 1560

gatacaacgc cagcaacccc ccaacaacag aaacaaaaac taaaaaattt agtactatta 1620

attttgacaa atccatttat ttcaataacc ttattcggac tatttttga tgatgaattt 1680

catggatttg atataataaa caaactggtt tcagcatggt tggatttgaa atgttggagt 1740

tggtttgtac tttgtatagg ttggcttcca tgttggctat tgatattagc gtcatcgttt 1800

gaatctaaat ctgtcgtagt aaggtcgaaa gaaaagcaaa gttag             1845
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182

<210> 170
<211> 510
<212> DNA
<213> Saccharomyces cerevisiae

<400> 170

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tggatgtcgt acttctacag ctcttcagaa ttgtcaataa gactgtcgtt cttctgggtg   180

acactatctc taacacaaat catcacttca attgtggcct cggggttttt tcacatgaga   240

gggataggtg gcatggcagg gtggcaatgg cttttttga tagaaagaat tttcacttta   300

gtcatcggta tcagtgcata cttcttgatg gtaccctccg tagttcaaac gaagaaacct   360

tggagcaaga aaggatggtt cactgagagg gaagaaaaaa tcatcgtaaa caagattctg   420

agagatgatc cgacaaaagg ggatatgaac aataggcaag gtatgtcact taaaatgtta   480

tggcagggga taacagatta ctatatatag                                     510


<210> 171
<211> 609
<212> DNA
<213> Saccharomyces cerevisiae

<400> 171

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ctaaataaca aaaacgactt ggtacattgt ccctcaataa ctttatttga atcgatcccc   120

acggaagtgc ggtcattcta cgaagacgaa aagtctggcc taatcaaagt ggtaaaattc   180

agaactggtg caatggatag gaaaaggtct tttgaaaaag ttgtcatttc cgtcatggtc   240

gggaaaaatg taaaaaagtt cctgacgttt gttgaagacg aaccagattt ccagggcgga   300

ccaatccctt caagtatct tgttcccaag aaaatcaact tgatggtcta cacgttgttt   360

caagtgcata ctttgaaatt caatagaaag gattacgata ccctttctct tttttacctc   420

aacagaggat actataatga gttgagtttc cgtgtcctgg aacgttgtca cgaaatagcg   480

agtgctaggc cgaacgacag ctctacgatg cgtactttca ctgactttgt ttccggcgca   540

cctattgtaa ggagtcttca gaaaagcacc ataaggaaat atgggtacaa tttggcagcc   600


183

tacacgtag

<210>    172
<211>    1947
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    172

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agtttaaaga aatctgtgac agataatgac cagaataata acaacgtgcc caggaagaga   120

aaactagcat gccagaattg ccgtagaaga agaaggaaat gtaacatgga aaagccttgt   180

tcaaactgta tcaagtttcg taccgaatgt gtattcactc aacaagactt aaggaacaaa   240

agatattcta cgacttacgt agaagcttta cagagccaga ttcggtcttt gaaagaacag   300

ttgcaaatat taagttcctc gtcttccaca attgctagca atgctctctc ctcgttaaaa   360

aacaacagtg atcatggtga tgctcctaat gaaaaaatct aaagtatgg cgaaacagca   420

caatcagcac taccatcatc tgaaagcaac gatgagaatg agtctgatgc gttcaccaag   480

aaaatgcctt ccgagagccc tccaccagtt ggcacaaata gtatatatcc atcaaattcc   540

ttgtctataa taaaaaagaa gacggatgga agcacaagat atcagcaaca gcaggtcagc   600

ctaaaaaatt tatcaagaag tccccttatc ttaagatcgt tgtcactctt tttcaaatgg   660

ctatacccgg gacattacct tttcattcat agagaaactt cttaagtgc tttcttcggt   720

gatactaaca ctaaaagtta ctattgttcc gaagaattgg tatttgcaat cgctgcattg   780

ggatctttga tttcatacaa atcagaaact gagctttttc aacaatctga agtgttttat   840

caaagagcca agacgatagt actcaaaaaa atttttcaac tggaagattc ttcgttagct   900

gaatcgtcgt cctcttcgaa attagcaatc atccagactc tattgtgttt ggcattttat   960

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catttaatag cgatcctctt tggaagatca acttccttgc gtttgtccaa ttccactgtt  1200

ccagaaacag acgagctacc tgaaattgag actggtatag aggagtacat atatgaccca  1260

aaagtaatat tgtccactgc aaacccottg aagaaactga ttgtgttatc gagaataacg  1320

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gagatttttg catccaagat tttcagccca aacgaaactc tacttcaaag gagtgaatac 1380

ttggccaaat ttaatctgga ggtatacaat tggagaaggg atttgccccc tgaactacaa 1440

tggaccaaga ggtcattgat ggaaatgaca gattttaacc caaccatagc ttacgtatgg 1500

tttcattact atatcgtgct aatttcctat aataaacctt tcatatacga aatcaaacaa 1560

agccgggaat tggttgaagg ttatgttgat gaactgtatt atcttttaaa agtttggaaa 1620

aataaattta agacgtttga gaaggccaca atttacatga tttattctgc gatttttagcc 1680

atccaatgca tgaagtccaa cttgattaaa aaggatagaa aacaagactt cttaaatttt 1740

ttaagtgcgc ctaccctgaa ttacgaactt gctagaaaat tcatagaaaa ctctgaagat 1800

gctttgcata attcagaaac tatggattta ttagggactc tatctcacgg taacgatttt 1860

gccttagagt acaattttga ctttacttta ttgaatgaga ttgatatgct gattggtgga 1920

                                                             1947
aacaccaatg atggtttgtc gaagtaa
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<210>     173
<211>     1461
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     173

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aatcttcgtg tgaagggtga aaatttctac agagactcca agagagtcaa attcctgaat  120

atgtacacta gtgggaagga gatcaggaat aagaaaggta atttaattag ggccgcttct  180

ttccaggact ccacaatacc ggatgcgagg gtccaaccag atcgtcgttg gttcggtaac  240

acaagagtga tatctcagga cgcactgcag catttcagaa gtgcattggg tgaaacccaa  300

aaagatacat atcaagttct tctgagaaga ataagcttc ccatgtcatt gttggaagaa  360

aaggacgcag atgaatcccc aaaagccaga attttggata ccgaaagtta tgctgatgcg  420

tttgggccca agcccaaag aaagagacca cgtcttgctg catccaatct agaggacttg  480

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<212>    DNA
<213>    Saccharomyces cerevisiae

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aaggcgccaa tggttttagg tcatgaatca agcggacagg ttgtggaagt tggtgatgcc  240

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<212>      DNA
<213>      Saccharomyces cerevisiae

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188

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      176

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tcggaaatgc tatcaacgac ttctccgccc attttagatc atatatcgga tgacttaaaa     240

ctgaagcttt tcggctcgag ggatattcct tatagtcgtc ctatcgatac gttacaaaac     300

aacggaggtc ttggtactga taaaatcacg tctattaacg aaaaaacgta tgcattcagg     360

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gaatatatat ttggttctcc cgtaagatct tccgatttga cgcagtgcga caagataagg     540

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tggtcttcca tttcatcatg gttgacccag actcaaaaaa tgctcattgg tttcttgact  720

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agaataacaa attctatgaa gattgacctg ttaaaggcgg attacacaag aagtctatta 2160
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190

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<212>      DNA
<213>      Saccharomyces cerevisiae

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cactcgtcga ccccttctc tgccgatggt tcgctagctg tgttcgtac tgacgactgg  240

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<213>      Saccharomyces cerevisiae

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gatttgagaa ctcaaaactg gaagttgcaa aaggaggctg gtgttgatat catcccatcc  180

aatgacttct cctttacga ccaagttttg gatttgtctt tgttgttcaa tgtcattcca  240

gaccgttaca ctaagtacga tctatctcca atcgacactt tgtttgctat gggtagaggt  300

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gctgctgccc tagaagctaa cgctaaatct gttgaatcca gaggtaaatc caagtttatc 1200

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192

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accatcttga agagctaccc agctgaaaag ttctgggtta acccagattg tggtttgaag 2220

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<212>      DNA
<213>      Saccharomyces cerevisiae

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acggaagtgc ggtcattcta cgaagacgaa aagtctggcc taatcaaagt ggtaaaattc  180

agaactggtg caatggatag gaaaaggtct tttgaaaaaa ttgtcgtttc cgtcatggtc  240

gggaaaaatg tacaaaagtt cctgacgttt gttgaagacg aaccagattt ccagggcgga  300

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cacatgtttt tgttactaca cgtagatgag ctatcgattt tttctgcata ccaagcaagt  660

ttacctggcg aaaagaaagt cgacacagag cggctgaagc gtgatctatg cccacgtaaa  720

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<210>      180
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<212>      DNA
<213>      Saccharomyces cerevisiae
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<400> 180

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cctccgaagc aaagaagacc acactcaaaa tcgtttggtt ctactccggt tcctccggat 1500

gttattgcta gtaataaaag aagaacgagt ttattcccgt ggttacataa accgggaatt 1560
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194

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cccaaacagc attatctgcc aattcctcga atgaacagat cgttgagtgg aaacagtacc 1740

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gctgatcaat tagaattact aagtaacact catagcaata atgagcgcag taatgctta 1860

ccattaaccg aagatgatgg ggatgaaaga aattcaagat cacgcaagag ggaatcatgg 1920

tttcaaagac taacaagccg ttcaggctct gctaacaggg cttga          1965


<210>      181
<211>      669
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      181

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aactcggtga ttagcaaaca caacgcagca gaaggtttat ccactgaaga cctgttacag  180

gatgtcagag acgcacttgc ctctcattac ggggacgaat acatcaacag gtacgtcaaa  240

gaagaatggg tcttcaacaa tgctggtggt gcgatgggcc aaatgatcat cctacacgct  300

tccgtatccg agtacttaat tctattcgga accgctgttg gtactgaagg gcacacaggt  360

gttcactttg ctgacgacta ttttaccatc ttacatggta cgcaaatcgc agcattgcca  420

tatgccactg aagccgaagt ttacactcct ggtatgactc atcacttgaa gaagggatac  480

gccaagcaat acagcatgcc aggtggttcc tttgcccttg aattggctca aggctggatt  540

ccatgtatgt tgccattcgg gttttttggac actttctcca gtactcttga tttatacact  600

ctatatagaa ctgtctacct gactgccagg gacatgggta agaacttgtt gcaaaacaaa  660

aagttctaa                                                          669


<210>      182
<211>      1563
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      182

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caatccctta gatctgtttt cgactttttt cgagcagaca taataacatt ccaagagctc   180

aagacggaaa aattgtctat ctctaagtgg gggagagttg atggttttta ttcttttatt   240

tctatccctc aaaccagaaa gggatattct ggcgttggct gctggattag aattccggaa   300

aagaaccacc cactatacca tgcattacaa gtcgttaagg cagaagaagg tataacgggt   360

tacttgacaa taaaaaatgg taagcattca gcaatctcct atagaaacga cgtaaatcaa   420

ggaattggtg gttacgattc tttagatccc gatttagatg agaaaagtgc actggaacta   480

gattcagaag gcagatgtgt tatggttgaa ctggcatgtg aatagttat tatcagtgta   540

tattgtcccg caaattcgaa ctcatcggag gagggtgaga tgtttagatt aaggttcttg   600

aaagttttat taagaagagt tcggaatttg gacaaaattg ggaagaagat tgtgctaatg   660

ggcgacgtaa atgtttgccg ggatcttata gacagtgccg atacattaga acaattctca   720

attccaataa cagatcccat gggtggaaca aagttagaag cacaatatag ggataaagca   780

atccaattta ttatcaatcc ggacacgcca catcggagga tatttaatca aatattggct   840

gattcacttt taccagacgc gagtaaaagg gggatactga tagacactac gaggctaatt   900

caaacaagaa atcgacttaa aatgtataca gtctggaata tgttaaaaaa tttaagacct   960

tcgaattatg gctcacggat agattttatc ctagtgtcct taaagcttga acgatgcata  1020

aaagcagctg acattcttcc ggatatattg ggctctgacc attgtcctgt gtattctgat  1080

ttagatatac tggacgacag aattgaacct ggtacgacac aagttcccat accaaaattc  1140

gaagcaaggt acaaatataa tttaagaaac cataatgttt tagagatgtt tgccaaaaag  1200

gatacgaata agaatctaa taaacaaaaa tattgtgtat caaaagtcat gaataccaaa  1260

aaaaacagca acatcaaaaa caaatcgctc gactcatttt tccagaaggt aaatggagaa  1320

aaagatgaca ggattaaaga atcctctgaa attccacagc aagctaaaaa aagaatctcc  1380

acgccaaagt tgaatttcaa ggatgtcttt ggaaagcctc ccctgtgcag gcatggggag  1440

gaatccatgc tgaaaacatc gaaaacttcg gccaatccag gtagaaagtt ctggatttgc  1500

aagagatctc gggggtgattc aaataataca gaatcatctt gtgggttttt tcagtgggtt  1560

taa                                                                 1563
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<210> 183
<211> 1770
<212> DNA
<213> Saccharomyces cerevisiae

<400> 183

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tatcaaattt acccagcaag tttcaaagac tctaatgacg atggctgggg tgacatgaaa 120

gggattgcct ccaagctgga gtacatcaaa gagcttggtg ccgatgccat ttggatctca 180

ccattctacg actcgccaca agatgatatg ggttacgata ttgccaacta cgaaaaggtc 240

tggccaacat atggtacgaa tgaagactgc tttgccttga tcgaaaagac acataagctt 300

ggtatgaaat ttatcaccga cttggtcatc aatcactgtt ccagcgaaca tgaatggttc 360

aaagagagca gatcctcgaa gactaatcca aagcgtgact ggttcttctg gagacctcct 420

aaaggttatg acgccgaagg caagccaatt cctccaaaca attggaaatc ctattttggt 480

ggttccgcat ggaccttcga tgaaaagaca caagaattct acttgcgttt gttttgctcc 540

actcaacctg atttgaattg ggagaatgaa gactgtagaa aggcaatcta cgaaagtgcc 600

gttggatact ggttagacca tggtgtagac ggctttagaa ttgatgtcgg aagtttgtac 660

tccaaagttg taggtttacc agatgctcct gttgttgaca aaaactcgac ttggcaatcc 720

agtgatccat acacattgaa tggaccacgt attcacgagt ccatcaaga aatgaatcaa 780

ttcatcagaa acagagtgaa ggatggcagg gagattatga cagttggtga aatgcaacat 840

gcctccgacg aaactaagag actttatacg agtgcttcaa gacacgaact tagtgagtta 900

tttaactttt cccacactga tgtggggact tcacctttgt tccgttacaa cttggtccca 960

tttgaactga aggattggaa gattgccctt gctgagctgt tcaggtacat taatggtaca 1020

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ggtgacgatt ctcccaagaa ccgtgttatt tctggtaagt tactctctgt gttgctaagt 1140

gccttgaccg gtactctata tgtgtatcag ggacaagagc ttggccaaat caatttcaag 1200

aactggcctg ttgaaaagta cgaggatgtc gaaatcagaa acaactacaa tgccattaaa 1260

gaagagcatg gggaaaactc agaggagatg aaaaagtttt tagaagccat tgcccttatc 1320

tccagggacc atgctagaac acctatgcaa tggtctcgtg aggagccaaa tgctggttttt 1380

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tctggtccta gtgctaaacc atggttttac ttgaacgact ctttcagaga aggcattaac 1440

gtcgaagatg aaatcaagga tcccaactcg gttttgaact tctggaagga ggccttgaag 1500

tttagaaagg cgcataaaga cattactgtg tacggatacg atttcgagtt tattgattta 1560

gacaataaga agttgtttag cttcacaaag aagtacaaca ataaaacatt gtttgcggct 1620

ttgaacttta gctctgatgc gacagatttc aagattccaa atgatgattc atcgttcaag 1680

ttagagtttg gaaactatcc aaagaaggag gtagatgcct cttccagaac attgaagcca 1740

tgggaaggaa gaatatatat cagcgaatga                                  1770


<210>      184
<211>      2196
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      184

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atggattttg tccttgatga tagaacggat gaagggttga atttgctgaa aaaagctgaa  180

atggaaactg gttcagatca aactatcttg actttggcaa gaggtgttat tgaatttctt  240

caagccactt tgagttttga aactgaagaa atgaaaagag ctgcaattac tttaggcaaa  300

gctgagcaaa tgtcctggaa aagtaagcaa aatgctgaaa agaccaattt taggagcagt  360

tcaatatatc ctcccggtac tgtctatgct gtaacatata ctgagtcatg tctgttgcat  420

gccttgttga tgttatttag tgaaagcatg atggaagcag ccaaggcttt gctaaagtta  480

aggagggctt atacaatgtt acaagatatc atggttactg tcaaaaaagc tgaacgatcg  540

aaaaattcga gctctccctc tccaagcgaa aagagccaag agtcatgcgg aagttttgtt  600

tctgcagaga caactttcat atcggttgat ataccataca aattgtcttc cgaggacaag  660

tccaatccac tcctattgga atttgctgaa aaaatctaca cgatgagaat gggaaggtta  720

tcaggtgccc atattggcaa tactccatct tttcataggt taagggatga tttgggttta  780

cagacgactc cgtctcaagc ttccgaccgc cattctgttt cagatgattt cgatttagaa  840

caggctacca tcgacgaatt catccattca ggtgctaatt tatgctatgg tatcttgcaa  900

gtcgtcttat ccttacttcc acctgcaatc ggtgctgtgc tatctattgt tggattcaag  960
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198

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ggatcccgtg aagaaggttt gaggctagtt tggaaggcta caaaggagag aaatgttcac 1020

gggtgtatag gtttgttagg tctgatgttt tattacgacg gtcctttcca atttacagat 1080

gctgactttg atataccacc aaacgataat ggatcgaggg ctttaaacaa aagcagaaca 1140

aacgatagta gccttttacc aggttatatg gacagtgcaa ccttattgca tcctggaaaa 1200

attctggagg acgcattact aaaagcaaga gcactttttc ctaatagtgc cctgtggctg 1260

ctaaatgagg ccaaaatgct tgctggaaag ggcaggcttc gtgattctct ggccctaatg 1320

gactctattg atgtcaatag tatccgtatg agacaagtga aatcgttgat ggtgtttgaa 1380

cgtgcgatcc ttttagtcaa cttacacgaa tacaacagag ctgccgatga tttaataagt 1440

ttgcttgata ttagtgattg gtctcacgca ttgtacactt attttgcggg ttgctgttac 1500

ttggaaaatt ggaggatgac acaattaggc ttattaaatg acggtaaaga acaattctat 1560

aaagagcggg ctcgagaact catatttgac gctccatctt tgttaggtaa gaaaacgttc 1620

aaatccaaaa atcttccatt ggatagattc atgcttagaa aagttcaaca atttaataat 1680

atgcagaaga aattaaacct acaagaacca ctagactcaa tagcaacatc acctgtccat 1740

gaactggctt atttctacaa cggttacaac aggatgactg aaaacgattt aattttgacc 1800

aaaaagatgt tgacagagta tcacaacccc gccattgatt cggaagaccc agatcaagag 1860

ctgatcagaa acttactact atccttgacc ttaagaagat tgggggatgc tgaaagaggt 1920

ttagccttgt tagatgacat tgttctgcca aaaatattct acattcaaaa tggcaaagtc 1980

aaatatttca aaaaaccga agacccatgg gcatatccag ccgctcttta tgagagagct 2040

ttattctgtt ggaaactggg tggcatggaa agtttgaatg aatgtaggga atggctgcta 2100

agagcccaaa attatgccgc cgattacgaa ttgagtacgc gtatcggtat gaagatcaaa 2160

gccgcccttg atagagttga aaacgcgctt gcttaa                             2196


<210>       185
<211>       2790
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       185

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199

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ttttcctcgg gcactgttcc tactttgggc aattcaccct acactacacc ccaattgaat  180

cagcaggatg gttttcaaca acctcaagcc tttaccccta agcaatttgg tggcttcaac  240

aacggttcgg gttccgttat gtccacgcct gtaatggtga gtcaagagcg attcggtgcg  300

agtgaggcct cctcgccata tggtcaatct atgcttgata tgacagcgcc tcaacctaca  360

tctcacattg ttccaactca aagatttgaa gatcaagctc aatatttaca acgatctttc  420

gaaacttgta gagattctgt tccgcccttg ccgaccaccc agttttattg tgttgaccaa  480

ggttcatgtg atccgcactt gatgagttta tccatgtaca acatccccga aagtgaacac  540

ttgagagccg ccacgaagct accacttgga ttaaccatcc aaccattttc cactttgaca  600

ccgaatgatg cagaagttcc cacaattcca ttaccaatgg atggtacgcc tttgcgttgt  660

agacgttgtc gtgcgtatgc taatcctaaa tttcagttca cttatgattc aagtgttatt  720

tgtaatattt gtagagttaa gatgcaagtt ccaggtgagc attttgcgcc catgggtccc  780

aatgggcaac gaagtgattt gaacgaaaaa tcagagttat tgcacggaac agtcgatttc  840

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tttttgattg atgtttcatt gttagctaat gagaacggaa gttctttagc catggtggaa  960

ggtgtcaggt catgtattga gtatatttca gatttccagc caaattgtga ggttgctata 1020

atcgtttatg ataataagtt gcggttcttt aatttgagac cagatttaga taatgcacaa 1080

gagtacattg taagtgaatt ggacgatgtt ttcttaccat tttataatgg attatttgtt 1140

aaacccggaa actcgatgaa aatcattaat gacacattga taaaaattag tggttacatc 1200

tccaccgaca agtatagtca cgtaccccaa gtctgttatg gttctgcttt acaagccgca 1260

aaattagcgt tagacacagt aactggcggg caaggtggta agattatttg ttctttgaac 1320

agcttgccaa cgatcggcaa cgggaattta tcgctaaaaa gggacaatgc acacattgct 1380

catgttaaat gcgacaatgg gttctataag aaattagcat cggatttttt gaaatcctac 1440

atttctttag atttatatgt gaccaatgcg ggattcattg atatggccac tgtgggccat 1500

cctgtagaga tgacttccgg tattttgaaa tattatcccc actttcaaca agagacggat 1560

gccttcactt tggttaacga catggttaca aatgtctcca atattgttgg ttatcaagct 1620

ttattgaaag ttcgctgttc tactgggcta tctgtggaac agtactactg cgattcatct 1680

gataatacgg atcatgatcc aattattcct gtattgacta gagataccac cttagatgtc 1740
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200

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tctaataaca ttcgtgaaat tttcaagttt ataaatcaaa atcctgtcat gagaataatg 1920

atcaaagatg tcataaagac gctcggtgat tgtgactttg taaagatcag aagattaatt 1980

gatgacaaga tggtcgaaat cttgacccaa tatagaggat tggttagcag taactcatca 2040

acgcaattga tactgccgga ttctataaag acattgcctg cttacatgtt agcatttgaa 2100

aaaagcgaat taatgaagcc aaacgctcaa agtacccgtg gtaatgaacg aatttatgat 2160

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gacaagaccg tcaacagaat cgaatcatat gacaattact tggtgataat gcataaaaaa 2700

attcaagaaa aacttcaaaa agacgatttc attaaagtct cgactgccgc aactcacgaa 2760

aatatccatc aaaaatttgt gcagttttga                                  2790


<210>     186
<211>     2694
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     186

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ccagctgttc atatcaaact cagtaaagag gaaaggtctc actacaggga gcaatacgat  120

tcattaaagt atatttcaaa ttatgtttct gttttcgacc aagcgttaag cgacaatatt  180

gactctagga ttagaaaaga aaatgaagcc ttactgaaaa aatattatga atcaagaaaa  240

ccttttactt ttaccagctt taggcaagga agtgtaatca gttcttctga ttcttctaca  300
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201

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ggcttcactg agagaacaaa gacctactgt tttttgaacg atttcgtcag taattgcgta  360

aatgaggtag atccatatac gctgaaaatg acagtaagaa atagaaacac tgccttgaat  420

atggagaacc tcgatgatga acgtaagagc aaagatgata tatacgattt tgaagataat  480

actgacgacg agtgtaatgc caagtgccat ggtgctttcc attattcgtc agaaagattg  540

gaaattcttc gctcacgttc gacaatatcg tactttaagt attataaaaa gcttttgacg  600

gtagacctaa gggacagtga tgttttaaaa aggcataatt tatggatgcc aatgatcact  660

agaagattta gatttttatt agtatcaagt tcgaaaccgg aagatgtaag gttaacaacg  720

ccgattccaa cattctcgga atcagattta gacattttca agaacaagac atgtccactc  780

tttatcaatg gtacagactg tgttcctaga agttatgaca ctttttcggg ttcttctgta  840

atcgcttcaa tattttcaga atataaactt ccatcccttt catatcattg ttctgtcgag  900

ttgaacgacc aattatttat tgtcggtggt ttgatggcat gtcatagata tgatgaggaa  960

gcgcctgatc taaaggattt ttacgtggat ggcataaaga atttaccgcc accactaata 1020

ccagagctaa ttaataaccc atccatgatt cctaatcctc acttgtactg tttttccttg 1080

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acccagggct gtaaattaac tgaaaggcat atcttttgt atggcgggtt tgaaatcaag 1200

tcggaaaccc aagttgatga taagggaaga tattttataa gaaaaagagc ttttttgaac 1260

aatactggtt acattctaga tacagtgacg ttcaatttct caaagattga attagtcgct 1320

cctccgtacc agtttgcaat ttacaataat ttctcgccaa gatttggtca catgcaggca 1380

tcaataagta attccaacaa caatgtatcc aatgaaaata ccacaacaag tgcgaaagga 1440

agaaggtcga taagcccata tcgccaaggt aatggggatc acaaaataga tgatttggtt 1500

ggttcaccag gaagtacgga ctatttagag gatgatgcaa ttccacctgt aacaaaccca 1560

aggtctacag atagtctctc ttccaaacat tgtagcacag caacacacat ttgctcatct 1620

gttaatacca ttctgatctt tggagggtat agtcagactg gtgacgacaa gtatgaagct 1680

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ccgagcagaa gagccttttc agcgtgctgt gtaccagatt attttaccaa ggatgttgaa 1860

cccatagaaa cgagattact gaggaacttg aaaaatgact ctccatcga tttggaaata 1920
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202

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aagaagagtg gtcgcgatag tatgcatatt tccaattcta ataatagtac tagtgaagac 2040

acttcttcaa agtctaccag gaataccaca tccagtcctc ccacaagccc taaacataca 2100

ccaccattga atccatcaaa aaaatgtgca tcaatcggaa gaactattgc gttccacgga 2160

ggttcagatg gctatgacgt ttgcagcgat atgtggtggt ttgacttcga ttccgaaacc 2220

tggactaaaa tagacctta tgccaaaaca caagaggaat ctgatggttt ggtacctatc 2280

aacttatgta tggtaggaca ctcaatgaca actgtaggcc acaaggttgt gcttatcggg 2340

ggtctacgac aaggtgatgt tgaccgaata taccgggacg aaactcttcc tgaagaagta 2400

atatcgggtg ttccactcgg aagtggcgtt ataaatgtcg tggatttaaa tacacaatgc 2460

cttcaaggtt gcaagctaat acgaaatgat ggagatacta aagaatctgt cattatggat 2520

cctcatgtcg gcacacccca ccaagtattg gccgtcgcag gtactataga actggtcaaa 2580

ggaaccatga ccttaatagg aggtgtagta gccggtcgcg aagacatttc gagcctttac 2640

ttgagaggag ctgtcttaca attcattcta ccaagcatga atctagccaa ctaa       2694


<210>        187
<211>        978
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        187

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caatattggg tgacatttgc tccatctttg gcacttaagc cagacgctaa caagaatagc  180

gattcaaagg cggaggaccc gttcgccaat cccgacgaag aactagtggt gactgaagat  240

ctaaatggtg acggagaata taagctgcta ctcaacaaat ttcctgtggt ccctgaacat  300

agtctcctag tgacaagcga gtttaaagac cagagatctg ctttgacgcc aagtgacttg  360

atgactgctt ataatgtgct ctgttctctc caaggagaca aggacgatga tgtcacttgt  420

gaaaggtatc tggtctttta taattgtgga cctcatagcg gttcctcaca agatcacaaa  480

cacttgcaga tcatgcaaat gcctgaaaaa tttatacctt tcaggacgt attgtgcaac  540

ggaaaggatc atttcttgcc caccttcaac gcagagccat tacaagatga taaggtttcc  600
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203

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gctatgtgtt acgtatcttt gatgcagaga gcacttacat ttttccaaga ttggaccaat   720

gagtctccgg agttgaccaa gtcatacaat gtgctactga ccaagaaatg gatctgtgta   780

gttccaagat cgcatgccaa gagtggaccg ccattgatgt taaacattaa ctccacgggg   840

tactgtggta tgatcctcgt taaagacaga gaaaaactag agaacctcac tgaagatcct   900

catcttgtgg acaagtcgtt actgcaatgc ggtttcccca acacagcagg ccaaaaacca   960

acagagtatc actattaa                                                  978


<210>      188
<211>      648
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      188

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cctatgcagt cacttctttt ttatgtgaaa gagtatagaa aagacagtga tctccaatgc   180

tctatcaaag aacttttgaa acctttggag ttcgaattca gcccaaggc cgtcagaggt   240

ttacactatt cagaggattt caagaaaaaa ttagagtttt tgaaatatca ggaacaagaa   300

cttgaatatc aaagtatggt caagagaagc aagtctgtct tttcacttca agaagacgat   360

gaactcacgc cttcacaaat taataaacag attaaggaac aagttaccac tgtttttcaac   420

gttcttgtaa gtgtcatatc ggttgttgtg gccatttggt actggaccgg atcttcaaca   480

aactttccgg tccatgttcg tcttttgttg tgcttgttct ttggaatatt ggtcttagta   540

gcagatgtgg ttgtgtataa cagctatctg aaaaaactcg aagaagcaaa agtaaaagaa   600

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<210>      189
<211>      1980
<212>      DNA
<213>      Saccharomyces cerevisiae

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atgacagggg gcgagccaat tgacccaaga gatctcgatt gggacgggcc cgatgaccca 240

gacaatccgc ataattggtc ctctttgaag aaatggtata ctactatgac ttcagctttt 300

cttttgtttgg tcgtcacaat gggtagttcc ctatatgttt cttccgtacc agaattggta 360

gaaagatatc acgttagtca gactttggcg cttgctggtt aactttcta tcttctgggt 420

ttatcgactg tcatcggcgc tccattaagt gaagtgtttg gtcgtaagcc tgtctatttа 480

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agaataattc tacccctaag gtttttatca ggtgtctttg catcccccgc cttatccgtt 600

ggatcaggta ccatcctgga tatctttgac gtggaccagg tctccgtcgc aatgacatac 660

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205

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ctatctctgc gcaggaccca tacgcagccc gttcctgcct cgtttgatcg cgaggacggg 1860

caacatgcgc aaaatcgtaa tgaacccatt tccaatagtt tatactcagc tatcaaggat 1920

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<211>        1668
<212>        DNA
<213>        Saccharomyces cerevisiae

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gtgcatggaa aagccccgat gctaatggcc aataatgatg tttttactat tggaccttat   180

agggcaagaa aagatagaat gcgggtatct gtcttagaaa agtacgaagt tattggctac   240

attgctgcgg gcacatatgg taaagtttac aaagcgaaaa gacaaatcaa ctccggtacc   300

aattccgcta atggttctag tctgaatggt accaatgcga aaattccgca gtttgacagc   360

acgcaaccaa aatcaagctc ttcaatggac atgcaggcaa atacaaacgc attaagaaga   420

aacttgttaa aggatgaagg agtgaccccc ggaagaatac gaactacgag ggaagatgta   480

tccccgcact ataattccca aaaacaaacc ctcattaaaa aaccgctgac ggtattttat   540

gccattaaaa agttcaagac agagaaggat ggcgtcgaac aattgcatta tacgggaata   600

tctcagagtg cctgtagaga aatggcatta tgtcgagaat tgcacaacaa gcatttaacc   660

acattagtgg aaattttttt ggaaaggaaa tgtgtccata tggtatacga atatgcggag   720

catgatctgc tacaaattat ccacttccat tcccatcccg aaaaaaggat gataccacca   780

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aaaattggtg atttaggttt ggccagaaaa tttcataata tgctgcaaac cctctatact   960

ggggataaag tggttgtcac tatatggtac cgtgcacctg agttgctatt gggagcacgg  1020

cactataccc ctgcggttga tttatggtcc gttggctgca ttttgcaga actgatagga  1080
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206

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ccttatttgg agaagtatcc agaatatgat caaattacga agtttccaaa gtatagggat 1260

aaccttgcta catggtatca ttccgcggga ggaagggaca agcatgcttt aagcttactt 1320

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aagtacttca cagaaagtga tattcctgtt agtgaaaatg tatttgaagg tctaacttac 1440

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acgaaaaaca atacacaagc ttcaggaatc accgcaggtg ccgctgcaaa tgcgttaggt 1560

gggcttggtg ttaaccgtag aattctggcc gcggcagcag cagccgctgc tgcggtgtca 1620

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<210>    191
<211>    597
<212>    DNA
<213>    Saccharomyces cerevisiae

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caccaatcaa gaccccacca aaggccctcg acaatgccag caacgtcctc atcccaaaca   180

tatgctcact cacactctta tacgcctaca agttcccaac cacggcctcc accgaggcca   240

caacagaatc ctagcttgcc ctggacatac cctcccaggt tttactgttc caagtgtgga   300

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atatgtcctc tttgtcatgg tgtaggcaga attatcaccc agcctcaacg ctattag       597


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<212>    DNA
<213>    Saccharomyces cerevisiae


207

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tcacctttg	agagagttaa	aatactgctg	caagttcaaa	gttcaaccac	ttcttataac	180

cgaggtatct	ttagctctat	acggcaggtt	taccatgagg	agggaaccaa	aggtttattc	240

agaggaaatg	gtttgaactg	cataagaatt	tttccctata	gtgcagtcca	gtttgtagta	300

tacgaagctt	gtaagaaaaa	gttattccat	gtaaatggca	ataatggaca	agaacaacta	360

acgaacaccc	aaagactatt	cagtggtgca	ttgtgtggtg	gttgtagtgt	ggtggctact	420

tacccgttgg	acttgatcaa	aacaagacta	tcgattcaga	cagcaaattt	gagcagttta	480

aaccgctcaa	aggcaaaaag	tatatcaaag	cctccgggga	tctggcaatt	actaagcgaa	540

acttacagac	tcgaaggcgg	tctcagggga	ttatataggg	gtgtatggcc	aacgagtctt	600

ggtgttgttc	catatgtagc	actaaacttt	gcagtttacg	aacaattgag	agaattcggt	660

gtcaattcct	ccgatgctca	gccttcctgg	aaaagtaacc	tctataaatt	aacaattggc	720

gccataagtg	gaggggttgc	gcaaacaatc	acttatccct	ttgatctgct	aagaagaaga	780

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gcgctcgtga	caatcggcag	agcagaaggc	gttagcggtt	actacaaagg	cttagctgca	900

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<211>	3303
<212>	DNA
<213>	Saccharomyces cerevisiae

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aatcatctta	atgaggtgga	aaatgaagat	agcaaagttt	tagatgacga	tgcagtgtta	180

taccctctta	tacctaatga	gccagatgac	atagaaacgt	ctaagcccaa	tattaacgat	240

attaggccag	ttgatattca	attgacttta	ccattgccgt	ttcagcaaaa	agtggtagag	300


208

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attgtggcca atttattgca tgttttagct acaccaacat ccattaacgg acaactaaag   420

cgagcgctcg tcctagtgtt gaatgcaaaa cctatagata atgtaagaat caaggaggcc   480

ttagaagagc tgtcgtggtt ctctaatact gggaaggacg acgacgatac tgctgtcgag   540

agcgatgatg aacttttttga aaggcctttt aacgtagtta ccgcggactc gctgagcatt   600

gaaaagagaa gaaagctata tatttctggc ggaatcttga gcattacttc tagaattctc   660

attgtggatc tcttatccgg cattgttcac ccaaataggg ttacgggtat gctggtattg   720

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aaaaatactt ggggttttat taaagccttt tctgaagcac cagagacgtt tgtcatggaa   840

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aggttcaggg tagaggtctc ttcctgtttg aatgccacta ataagacgtc acacaataaa   960

gtcattgaag tcaaggtctc cttaacaaat tccatgtctc agatacagtt tggcttgatg  1020

gaatgtttga aaaatgtat tgctgagtta agcagaaaaa atcctgaact agctctggac  1080

tggtggaata tggaaaatgt cctggatata aactttatca ggtcaattga ctcggtgatg  1140

gtgccgaact ggcaccgaat ttcttatgaa tcaaaacaac tggttaagga tataagattc  1200

ctacgccacc tttttaaagat gctcgtaact tcagacgcag ttgactttttt tggagagatt  1260

caattaagtt tggatgccaa taaaccgtca gtatcccgaa aatacagcga atcaccgtgg  1320

ctattggtcg atgaggcaca attagtcata tcgtatgcga agaaaagaat attttacaaa  1380

aatgaatata ctttagaaga aaatccaaaa tgggaacaac ttattcatat attacatgat  1440

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cgtcaagtgc ttctgaataa attgaaatgg tacagaaaac agagggagga aacgaaaaaa  1620

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gttgcggccg ttgaaaagct aaggaatgca ggtaccaatg tagatatgga ggtggttttt  1800

gaggatcata agttatctga agaaattaag aagggaagcg gtgatgattt ggatgacggt  1860

caggaagaaa atgccgcaaa cgattcaaag atttttgaaa tacaagaaca ggaaaatgaa  1920
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209

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tatgaatatg ttgatcgtca ggacgaaatt ttaatctcta cgtttaaaag tctcaatgac 2100

aattgctcat tgcaggagat gatgccctct tacattataa tgtttgaacc agatatatcg 2160

tttatcaggc agattgaagt ttataaggcc atagtgaagg atttgcaacc aaaagtatac 2220

ttcatgtact acggtgaaag tattgaagag caaagtcatt tgactgctat caagagagag 2280

aaagatgctt tcacaaagtt gattagagag aatgcaaatc tgtcccatca ctttgaaacg 2340

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cgaaaatcta ataccagaaa tgcgggtggg cagcagggat tccataatct tactcaggat 2460

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aatgagatta atgaacttat taatgacgaa gatttgacgg atagaatata ctacttcttg 3180

agaacagaaa agaagaaca agaacaagag tcaacagatg aaaatcttga atctcctggt 3240

aagaccactg atgataacgc tttacatgat catcataatg atgttcctga agcacctgtg 3300

taa                                                                 3303


<210>      194
<211>      3108
<212>      DNA
<213>      Saccharomyces cerevisiae
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210

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gctgaaaacc cgtaccagaa gacgaccata ttgcataatt ggttgctaag ttacgaattt   180

cccgctactt tgattgcatt agttcccgga aaggttatta taattactag ttctgccaag   240

gccaagcatt tacaaaaggc aattgatcta tttaaagacc ctgaaagcaa aattacgctg   300

gaattgtggc aaagaaacaa taaagaacca gaactcaata aaaagttatt tgatgacgtt   360

attgccttaa tcaatagcgc tggtaaaaca gtgggtatcc ctgaaaagga ctcttaccaa   420

ggtaaattta tgactgagtg gaacccagta tgggaagcgg ctgtgaagga gaacgaattc   480

aatgtcattg atatttcgct gggtctttct aaagtttggg aagtgaagga tgttaacgaa   540

caagccttcc tgtccgtttc aagtaagggg tcggacaaat ttatggacct tttatccaat   600

gaaatggttc gggcagttga cgaggagttg aaaatcacca atgccaagtt atcagacaaa   660

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gtttatgaat cagtaataga atacatcgaa aaaaccaaac ctgaactagt gcccaatttc  1080

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caaaagaagc tacacgaaaa attggaaaag aatggattac tcagatttag tgctgctgat  1560


211

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caatttgtac gttcgattac actaagatcc aaagatggtg accgcatgag tgaaaccttt 1920

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gctgatgttg ttcaacagga caaattgatt gaaaataaaa ctggaagaac gaaaagactg 2040

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tctaacgagg ccaacaatag gagatcactt tatggcccca atgaaataac cgtagaagat   240

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ttaataggat ccgcagtggt ctctcttttt atgggtaaca ttgatgatgc tgttagtatc   360

acactggcca ttttcatagt tgtcactgtc ggttttgtcc aagaatatag gtctgaaaaa   420

tctctagaag cgttgaataa attggttcct gctgaatgtc acttaatgag atgtggtcaa   480

gagagtcatg tactggcttc caccttggtt cctggtgatt tagtgcactt cagaataggt   540

gacagaatcc ccgcagacat tagaattatt gaagcaatcg atttatccat cgatgaaagt   600

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tcctttggtg ccgtttttga aatgatgaat aatattgaaa aaccgaagac tccattgcag   840

ttaacaatgg acaaattggg aaaggacttg tcactggtta gcttcatagt tattggtatg   900

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213

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215

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216

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218

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219

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220

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224

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225

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226

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<213>     Saccharomyces cerevisiae

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cagactccag tctctccgag tgcgacgcat gctcctgata cttccaataa tcctactaat  360

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<211> 1515
<212> DNA
<213> Saccharomyces cerevisiae

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231

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cggttgtcac atctgtccac ggacttggtt gcgacagcgc agtctgtgct tggtttggaa  240

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ccggagttgc ctaacaaaga cgtgaagctt gatctcgagt atttgagcag aagatcgacc  540

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<213>      Saccharomyces cerevisiae

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233

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gctgtgaagt tcagccctga tgggagactc tttgcattag cctcaggcag gtttttacag  360

atttggaaga ctccagatgt taataaagac agacagtttg ctcccttcgt ccgccatagg  420

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accaagaggc catccgatga cgacgacaat gaaagtgaag acgacgacaa gcaagaagaa  720

gtagatattt cgaaatacag ctggagaatc acaaagaaac attttttta cgcaaaccaa  780

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234

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<213>    Saccharomyces cerevisiae

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ccccaccata gtgatgtaac atgcagtaac gcacggcggg ccgaaagtcg gactttaccc   180

cagatttgta gttgtatcct attggatcac gggcgacgga caagacccga agtgcggacc   240

ggcatggtca gcttgcacgg aagctttaag ggtttccctt gtttcggcat tagaagaggc   300

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<213>      Saccharomyces cerevisiae

<400>      212

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agttcttttc aatcctcttt taatactgac caaaaaagcg cgaacaatgg aagtactgtg   180

agaagaagca taaggtcgat ttttagaaga gcagccgaat tgcctagagt ccatatgggg   240

cctcttactt attcacatgg gataaatgag cttgttaaca agaaattaag aaaagactgt   300

gatctcagca cgctatgtcg cgtattgcaa agaggaatca ggatgattag gatgacaaga   360

agaagaagga agttctatga atttaaatta atcaataaca acgggcaaat aatatggaaa   420

gatggttcga agtatctgga attagactcc gttaaagaca tcagaatcgg tgatacggcg   480

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gctattattt ataaggtttc caacaaattg aaagcgttac acgtagttgc tttgaatgaa   600

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ttaaagaata ggaaagaggt aaatatgatt tggtctaaat ttacaaaacc tccacactcc   960

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caagatggtt ttaccaagtt cttgaaggag caaccatatt tggtggaggt aaagaggag   1140

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gggaaacaaa ttgcagaaac tccatctgtg gagggatata ttcaagtcct acaacaaggt  1260
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236

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<213>      Saccharomyces cerevisiae

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cgtcgtggtg gttacggcaa cggtggtttc ttcggtggaa caacggtgg cagcagatct    240

aacggccgtt ctggtggtag atggatcgat ggcaaacatg tcccagctcc aagaaacgaa    300

aaggccgaga tcgccatatt tggtgtcccc gaggatccaa atttccaatc ttctggtatt    360

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gcctttttca acagtgaaaa cagtaacatt gttaaaggtt tgcatgaaat tttgactgaa   1560

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238

agcaacagcc gtagaggcgg tttcggtcgc aacaacaaca gagattaccg taaggccgga 1680

ggcgctagcg caggcggctg gggctcttca agaagcagag ataactcttt cagaggcggt 1740

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<213>      Saccharomyces cerevisiae

<400>      214

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agggccactc accccggaaa tattccaaat aaggagtggg ctgctgtgta ttatggtcag  180

cgtgctcaaa gacctggtac catgatcatc acggaaggta cgtttatttc ccctcaagcc  240

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ttagaagagg gcctgccatt gaacaagtat gacagaagta ccttctacac catgtccgcg 1140

239

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tga                                                                1203


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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      215

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tatgtatacg aacagtatga tactgaagat dacaaggtaa tgcatcattc tatacgtgtc  180

attctgaacg aggcgcgctt tcctttttttc ttttttgcttt ttctttttttt ttctcttgaa  240

ctcgagaaaa aaaatataaa agagatggag gaacgggaaa aagttagttg tggtgatagg  300

tggcaagtgg tattccgtaa gaacaacaag aaaagcattt catattatgg ctga         354


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<211>      1575
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      216

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agagatgaga aaggtgattg caatgaagaa aaggattctt ccaaagattt ggggagggta  180

ccgtcgaaga tgaaacgagc atatgatggt gaaacagtta ttaaagaggg agattcgcat  240

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attattgagg acttacaaag aacaagtttg agagaaagca ttcatagtat ggaacagtta  600

ccatcttcgc acaaacgtaa acccgtaata ccgtgggacg catctataag tggcatggtt  660
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tcaagtgcaa atacaagtaa aagacagaaa atgttaaaag caagaagcga ctttgaacat    960

aaacagaaaa attatgcata caaacacaca tttatcaaaa atgatcagga actgttccgc   1020

aatgaactaa ctaagttaaa taagatactt gctagagaat caaaaaatt gacaaagcta   1080

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aagagaatgc attggttaag atacaccaag aggcacaata ccttttgggg gaggactata   1440

cataaggacg ttcaagtcag cttcaatgac aagtatgttg ttactaggag cggcgtgagg   1500

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gactactatg agtga                                                     1575


<210>      217
<211>      1557
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      217

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tctaccggtt cccgagtaca tatatacaag tttgacgtct gtacttcccc acctacatta    360

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241

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gccaaatctt caaaaatttt gagcgctgta agggatcatt tggagaagga ctatcctttc    600

ccagttgtcg aaggtgatgg tgtttccatc atgggcggtg atgaagaagg tgtcttcgcc    660

tggattacta caaactacct attaggtaat atcggtgcta atggccccaa gttacctact    720

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ccaccatgct ctttcaatgg ggttcaccaa ccttctttag ttcgtacatt caaagaatcg   1200

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<213>    Saccharomyces cerevisiae

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ctggctggag cagcaactct gttagagaca ataacgttct tgatttcagt caatggttcg    180

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242

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acaccaacaa cgaacaaaga cttgtattct tccaagtatt ctcttaattt agcaaagtat  420

tcagctttct tttcacgaat gcctcccatt tcaaacttat tatacgtatt tattagactg  480

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atcgagaatt ag                                                     552


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<212>      DNA
<213>      Saccharomyces cerevisiae

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243

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244

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ccaagtttca taaaaccaga taatcattta gatttggata gtccctcgtg cactttaaag 1920

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cacggaagat ttgagtttgc tgagtttaac ttatgtaata aatcctacct tttgaaatta 2040

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cattttacac caagccggtt gtcaattcgt tcatcatcag gtcattatac ctataacact 2160

gactaccagg ttcttgaatg gtttcacgag cctggccatc agttcattga aatttgcgca 2220

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<213>       Saccharomyces cerevisiae

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gacggtggca atttcccaat gtatattgcc attaatgagt attttaagcg aatggaagat  180

gaactagata tgaagcccgg tgacaagatc aaagtaataa ctgatgacga agaatacaag  240

gatggctggt attttggtcg aaatctgaga accaatgagg aaggtttata tccggtggtc  300

tttactcaaa agataacagt ggagaaggct ccgacattga tgagagccaa gtctaccaaa  360

aggatatata gtccattaac caatgaagat cctcttcttt ccagcacttt tatcagtgaa  420

aacgattcaa acagtgaact gccaaccccg caaccaattg aaaccgccgc ctctatttcg  480

agaactgcca atggaaagat cgaaagaaac ttgtctttaa agaatacaat gagtgacata  540

gacaatgcac tactggagtt taaagacgac tctataggtc caccagatcg tttcatcaat  600

tcgggcagag acgaggaaca tagcattacg catgaaacaa ttctatcagc cactgatgga  660

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taa 3123


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<211> 2682
<212> DNA
<213> Saccharomyces cerevisiae

<400> 222

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agtgtttttc ccatcatcaa ctggctacca cattacaatt ttagctggtt tactgcggat 420

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gtcgccacgc taccagcgca gtatgggttg tactcctcgt ttattggtgc ttactcctac 540

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248

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<213>      Saccharomyces cerevisiae

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agaatattgt ttgtctgcca ggcttgttgg aagtcaaaaa caaagtgtga tagagaaaaa 240

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250

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251

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<213>      Saccharomyces cerevisiae

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<213>     Saccharomyces cerevisiae

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tttcgaaatg atctacgttt atatgataat gtgggactgt acaaaagtgt tgcgctcttc   300

cagcaattga ggcaaaaaaa cgcaaaagcc aaattatatg ctgtttatgt catcaatgaa   360

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gatgcccaac catattttag agttttaat atggatatac aagcaaaaaa atatgaccca  1560

caaatgatat tcgtcaaaca atgggttccc gaattgattt cttccgaaaa taagcgtcca  1620

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<213>      Saccharomyces cerevisiae

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254

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atagaaagca acatagctgc aggagaacca tctccatcga aaagaagatt tacacataaa  240

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gaaaaggcca tagatgggaa caatattaac gaggaaacaa ttgagttaga cgagttatct  360

cctcaaggga aaaccacctc tttcaataag aattttatac gtaagaaatt ctttgaatca  420

cgcagctcat ctgtgagtag cgagggaaag acgctcttca gttcttatga tacattcgta  480

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gacgtgtttg ctgacactac cgacaatacc gccctcttga attattcgca atttaacatt  840

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cagttgaaat cttttatcga attgaacaga atgggtttca gtaaaattac taagaagtct  960

gataaagtat tgcacatgaa cactaggcaa gaattaatag aaagtgaaga atttttcaaa 1020

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255

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256

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257

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258

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259

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262

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263

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266

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267

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268

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ctcgatttct ttggtagttg gggtgtcgag cattttttca agtttttctt catggacgac 3600

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<211>      1659
<212>      DNA

269

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aagaaaaatg tcattccgtt ggcaagcaaa atggaagttg gctcgaatga ggatgtgtct   180

agtatgggta atttcataaa taaattctac acagagtatt ctttaccctc acataaggta   240

ctgcaatcac tgcgagtcct tttttcatta gcaatgatga cgtatacagt aaccatagag   300

attattctat ggcagattaa ggttgctgga atggacaagg aagttacttt cataacgact   360

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aacaataaca gtaaatctct cttatggaca acagacgcct atatagagga aaaaatccaa   780

gattatgaac acaacattga acaaaatgta caaatattaa gaagtttaga agaagaggtc   840

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agtgaaaatg cagcatccga tcctttagcc attacgatag caaatatttt ggattttttcg  1140

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ggcgtctacg ttttggctac aacgctaatg gttaggtccc atctcccttt tgaagtatca  1500
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270

caaagattaa aggagctatt gggtggaaag tttaccgtcc caaacattgt catagattct 1560

tggtttgatg aagtctacgc ttttgcatgt gtgtttacct ttatttgcat aagaattgca 1620

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<210>      235
<211>      2121
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      235

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aactccatac ggagcacctc taattcgggt tctcagtcga tttctgcatc ttccactaga  180

agtaactccc cactaagatc cgtatcagcc aaatccgatc ccttccttca cccaggtagg  240

ataaggatca ggcggagcga cagtattaac aacaactcga gaaaaaacga tacatatact  300

gggtcaatca ctgtgaccat ccggccgaaa ccacggagcg ttggaacttc ccgtgaccat  360

gtggggctaa aatcgcccag gtactctcaa ccaagatcca actcacatca cggtagcaat  420

acatttgtta gagacccctg gtttattact aatgacaaaa caatagtgca tgaagaaatt  480

ggagagttca agttcgatca tgtttttgct tcccattgca ctaatttgga agtttatgaa  540

agaaccagta aaccaatgat tgataagtta ttgatggggt ttaatgccac catatttgcg  600

tacggtatga ccgggtcagg taaaacgttt acaatgagcg gaaatgaaca gagctaggc   660

ctaattcctt tatctgtgtc gtatttattt accaatatca tggaacaatc aatgaatggc  720

gataaaaagt tcgacgttat aatatcgtac ctcgaaattt acaatgaaag gatttacgac  780

ctgttagaaa gcggattaga agaatccggt agtagaatca gtactccttc aaggttatat  840

atgagcaaga gcaacagcaa tggattgggc gtagaattaa aaatcagaga tgactctcag  900

tatggggtca agttatcgg tctcaccgaa agaagatgtg aaagtagtga gaattattg   960

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agctcacgat ctcatgccat tgtactgatt cgtttaacaa gtactaacgt aaagaacggc 1080

acctcaagat cgagtacatt gtcgttgtgt gacctagcag gttcggaaag ggctacgggg 1140

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gagaattgtg aaaaactact agataaagat gtggttgatt gcaagattc tgagattatg 1800

gaaattgtag aaatgcttcc ctttgaggtc ggcacccttt tggaaacaaa gttccaaggt 1860

ttggaatcac aaataaggca atataggaaa tacactcaaa aacttgaaga caagatcatg 1920

gcgctagaaa aaagtggtca tactgcaatg tcgctaactg ggtgtgacgg cactgaagtg 1980

atcgaattac agaagatgct cgagaggaag gataaaatga ttgaggccct gcagagtgcc 2040

aaacgactgc gggatagggc tttgaaacca ctcattaata cacagcaatc accgcaccct 2100

gtcgtggata acgataaatg a                                       2121


<210>      236
<211>      1137
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      236

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aattatgtgt attttctacc ctcagctgtc cgtttgacgg tttcaaagga ttataccaag  180

tcgatcctgc cgttaaaaaa tgttcttgat agtggtattg aagttatcaa agatacggct  240

gccagctttg atgataagga ggtagttttg gggtcagaca gggccataaa gtttgatatc  300

ttggttcttg caactggctc aaagtgggct gatccaattg gttcaactta taccttcggg  360

gataactata aagagtattt tgaaagagag gcttctcgaa tctcagatgc agatcacata  420

cttttttcttg gcggtggctt tgttaattgt gaactagctg gtgaattgtt attcaagtat 480

ttggaggaga tcaggtctgg caaaaagcgt atttccatta ttcataattc cgataagcta 540

ctgccggact ctgggttata caacgatacc ctaagaaaaa atgtgacaga ctatctctca 600

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gttggtattt ctccaaatgt gccggtcaac agtatttcag acctttgtga caagaaaggg 780

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gttttgaccc gaaatgttat aagttcttta caagaaggaa cagaggctag tctcgttgat 960

gcagattgtc ttgagacagg acatgcccca agtggtgtct cccttgggcc aaatgcaggg 1020

tttggccaat ttccactacc gttacttggg acgattaata ttccatcgtt tttaatttct 1080

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<210>    237
<211>    1047
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    237

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tctggtgtct gccacaccga tttgcacgct tggcatggtg actggccatt gccaactaag 180

ttaccattag ttggtggtca cgaaggtgcc ggtgtcgttg tcggcatggg tgaaaacgtt 240

aagggctgga agatcggtga ctacgccggt atcaaatggt tgaacggttc ttgtatggcc 300

tgtgaatact gtgaattggg taacgaatcc aactgtcctc acgctgactt gtctggttac 360

acccacgacg gttctttcca agaatacgct accgctgacg ctgttcaagc cgctcacatt 420

cctcaaggta ctgacttggc tgaagtcgcg ccaatcttgt gtgctggtat caccgtatac 480

aaggctttga gtctgccaa cttgagagca ggccactggg cggccatttc tggtgctgct 540

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attgatggtg gtccaggaaa ggaagaattg tttacctcgc tcggtggtga agtattcatc 660

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gacttcacca aagagaagga cattgttagc gcagtcgtta aggctaccaa cggcggtgcc  720

cacggtatca tcaatgtttc cgtttccgaa gccgctatcg aagcttctac cagatactgt  780

agggcgaacg gtactgttgt cttggttggt ttgccagccg gtgcaaagtg ctcctctgat  840

gtcttcaacc acgttgtcaa gtctatctcc attgtcggct cttacgtggg gaacagagct  900

gataccagag aagccttaga tttctttgcc agaggtctag tcaagtctcc aataaaggta  960

gttggcttat ccagtttacc agaaatttac gaaaagatgg agaagggcca aattgctggt  1020

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<210>    238
<211>    1692
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    238

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gctttgaatg gtattgccgg ttcttacgct gaacatgtcg gtgttttgca cgttgttggt  300

gttccatcca tctcttctca agctaagcaa ttgttgttgc atcatacctt gggtaacggt  360

gacttcactg tttttccacag aatgtctgcc aacatttctg aaaccactgc catgatcact  420

gatattgcta acgctccagc tgaaattgac agatgtatca gaaccaccta cactacccaa  480

agaccagtct acttgggttt gccagctaac ttggttgact tgaacgtccc agccaagtta  540

ttggaaactc caattgactt gtctttgaag ccaaacgacg ctgaagctga agctgaagtt  600

gttagaactg ttgttgaatt gatcaaggat gctaagaacc cagttatctt ggctgatgct  660

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ccagtttacg tcacccccaat gggtaagggt gctattgacg aacaacaccc aagatacggt  780

ggtgtttacg ttggtacctt gtctagacca gaagttaaga aggctgtaga atctgctgat  840

ttgatattgt ctatcggtgc tttgttgtct gatttcaata ccggttcttt ctcttactcc  900

tacaagacca aaaatatcgt tgaattccac tctgaccaca tcaagatcag aaacgccacc  960
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274

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ttcccaggtg ttcaaatgaa atttgccttg caaaaattgt tggatgctat tccagaagtc 1020

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gctaacactc caatgaagca agaatggatg tggaaccatt tgggtaactt cttgagagaa 1140

ggtgatattg ttattgctga aaccggtact tccgccttcg gtattaacca aactactttc 1200

ccaacagatg tatacgctat cgtccaagtc ttgtggggtt ccattggttt cacagtcggc 1260

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cacggtcctc atgccgaata taatgaaatt caaggttggg accacttggc cttattgcca 1500

acttttggtg ctagaaacta cgaaacccac agagttgcta ccactggtga atgggaaaag 1560

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ccagtctttg atgctccaca aaacttggtt aaacaagctc aattgactgc cgctactaac 1680

gctaaacaat aa                                                  1692


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<211>     462
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     239

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ttagttaaag cggatgataa attactagag caacattacg cagagcatgt tggtaaacca  180

ttttttcccaa agatggtatc ctttatgaag tctggtccca ttttggccac ggtctgggag  240

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gcaccaggta ccattagagg tgatttcggt attgacctag cagaaacgt ctgtcacggc  360

agtgattctg ttgatagcgc tgaacgtgaa atcaatttgt ggtttaagaa ggaagagtta  420

gttgattggg aatctaatca agctaagtgg atttatgaat ga                    462


<210>     240
<211>     858
<212>     DNA
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275

<213>        Saccharomyces cerevisiae

<400>        240

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ttttccacag atcaagagca aaatccatta aatgactacc agtaccagat caatattagg    120

gaactggagg agtattacaa caagacgatt ttaaacgagg ataacataca ggaaacaagc    180

agtgaaatat cttcggcagt ttcattctct ccaccaaaaa atacaaacgc tattcaaccg    240

gggctactgt atgatccaca gttaatgaac ccttttctcc catccgctca cctgaatagc    300

acggcaccta ctactttaa aaagaaacta gaggtacaaa taaatccgga ctatgtccca    360

aaatcttcac aattaccatt aacttcacag aatttgcaac agttgtctca acaaaagccc    420

aaaaatgatg cttcttttc atcagagaag gaatcctcag ctcaacctaa ggtgaaaagc    480

caagtgcagg aaactcccaa acaattatac aagacagagc tgtgcgaatc attcacttta    540

aaaggaagtt gcccttatgg cagtaagtgt cagtttgctc acggactcgg cgaattaaag    600

gttaagaaat cgtgcaagaa tttcaggacg aagccctgtg tgaattggga gaaactaggt    660

tattgtcctt atggcagaag atgctgcttc aaacatggcg acgaacga cattgctgtt    720

tacgtgaaag ctggtactta ctgtaacgtc tcttcgacta gcaaacaatc agacgaaaag    780

agaagcaatg gtcgcggctc cgccaagaag aagaatctaa atgttaaagt aaaggctttg    840

cagagaatga cctggtga                                                   858

<210>        241
<211>        4263
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        241

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tctatccaaa tggaattcat gctacggaag caggatccaa agactctagt tgcgctgctt    180

tcaaggggatt tatggtgttt cagtataaat gatgatccgg taccgacacc tcctgcgata    240

gaacataaac cagtgagccc agataaaatc ggaactttca ctgccgatta ttcaaagcca    300

aacttaccgc cacactatgc tctttttta aaagctttaa gaaggaaaat ttacattaat    360

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ttggcattag gttcacacaa taagctaata caatttggga atgcctgcat atcattaagc  420

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cctgcttcca agcaaggata cttgataacg ccaccaaaac atacagaact tctcttgacg  660

acgttaagtg tatctcatgg tataaactta caaataaaa aaaatttgaa atgggttgct  720

gttgttcctg acttaggaca tctcaacggc cacacaccta ctatagcttc gtatttaact  780

cccttacttg aagcaaagaa gctagtatgg ccgctgcatt taatcttcgc ccaaccagta  840

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tctgatgaag aagaaataa taacaataaa agcattaata aaaataacaa ggaaatgcat  1620

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gaaatgacct tgccaacgag tccattatat atggacccag gtgcgccact ccctgtggaa  1800

acaccccgcg atagacgcaa aagtgtgttc gctccactga attttaaccc cataatagaa  1860

aacaatgttg ataacaaata caaatctgga gggaaatttt ccttcagtcc gttgcaaaag  1920

gaggaagcat taaactttga tatttctatg gcggatcttt ctagctctga agaggaagag  1980
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277

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aacgatgcta atatcactag caataaggaa ggcttcaact ctatttggaa aattcctcaa 2220

aatgatatac cacagaccga gtcaccactg aagaccgttg attcatctat tcaacccata 2280

gaatccaata taaagatgac cttggaagat aataatgtta ccagtaatcc gtccgaattt 2340

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caagaaggtt taataacaac cacaatgtta cagttatttt ccactttcga tagattaaat 2700

ggcaatgata cgatctccaa attctataac atgaagcagc cgtacgtttt tgtaaagaaa 2760

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cgccctccaa atggaataaa aaacttcaaa tccttattat taagttcatc tttcaaagaa 2880

gattgtctgt catttgcgcc aactctatct caaacatata ttaatcaaga gttagggttt 2940

tgtgagttgc ttaaactaac taatgaagac ccgcccggac tgatgtactt gaaggcattt 3000

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278

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279

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taa                                                                 243

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282

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283

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286

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287

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atcgccattc ctaatagtga actaaatgcg ctgcttgccg aacagcagga cgaggaagga 2040

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atgccgacag tgaactccag taaactcaca gcaggaaatg ggaaacctga cacggagaag   180

cttacaggag aactaatttt aacatacgac gatttcattg aactgatatc tagctcaaag   240

actatttatt cgaagtttac ggaccattcg ttcaatttga accagatacc caagaacgtt   300

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gactttcgat ttctgaaatt ttacaaatgt tatcatgaaa atgaagagta tttgagttta   720

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289

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catgccaatt attactataa aagctgtcaa attgcgaaaa cattcattga tttggacaat 2640

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<213> Saccharomyces cerevisiae

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tatcaagaag ccatggagag caaaaagaaa tacaagccaa gaagtaaatc gttaaggttg 240

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atggaaatag ttgtgaaaag acagtacgac aacaaggaga tatatagtac taaaaagggg 180

ggtgcctatt caaatgagga tgaagatgcc aacttcctaa aaggagagga ggagcttatt 240

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290

ggaatcccct caatggaagt aattagcgag gaggattatt tgcgaaggga tcaatccgta    360

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gctgcgctgg caaagcagga cgaagcatat gcccgagagc aattaacggc ggctatcggc    480

cgccactgtc gtgtcacagt agacgggagc gctccacgtg aggccatttt acggtacgta    540

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ggcaaaaacg atgggcgcat aaatggggta acactgtttg ggcctgtggc gccgggtcac    660

ggatcgtttg tgcgtccgcg ggctgtggaa attctatcaa aagacgaaga atccgccgag    720

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<213>      Saccharomyces cerevisiae

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aattggacaa ggtgccacct tttcgacact tcggttatta tgttacacag ttttcatgag    240

gatggcgcct tgactaactt aattagtcat ttgccaacca ccacagttcc ccaatatcga    300

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taa                                                                  363


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<213>      Saccharomyces cerevisiae

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aagaaaagtg attttgatct ttcccatctt gagtacggtc caggttcact aataccaaac    180

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291

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ggagctttct atgccctgcc tgtttttcaa aaaaatatg gttctttgaa tagcaataca    420

ggagattatg aaatttcagt ttcctggcaa atcggtctat gtctatgcta catggcaggt    480

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292

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293

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<213>     Saccharomyces cerevisiae

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294

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295

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gaatgcactt ttgagcttca aactttactg atgacatgga ttggcatcct tcctgaagcc 3000

aaagatttat tctttaagat caagacaagg ctcgccatgg aagaagagga tagtgccgat 3060

297

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<210>      258
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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      258

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aatagagttg ctgaggaatt ctctgaatca agtaaaaagc aatggattgc gacgagtttt   240

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gccagaaacg tcacggaatt ctcaatagca agagccatat gtggtattgg tgcaggagga   420

ttgaatgcta ttagtagcat tgctgttagt gacatatgta cagcaagaga aaggggcgtt   480

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ggtgtattta tagaaaccat tggatggagg gctctttttg gtatccaagt acccgtgata   600

atgttgtgct cggtattagc aatcaaaaac attaatatta agctattcca tgttcctcct   660

atgaaagaaa gatatacctt aaagaatctg tcacggatag atatatttgg ctcattaagc   720

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298

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attacattca gatctaactc aatatggtgg aaattgatat atgtgtttgc atcagtcctt 1260

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<213>      Saccharomyces cerevisiae

<400>      259

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aataatggcg gctttcagca gaaggaaaat gacatatttg aactgaagga cgttgatgac  360

caaaatcaga ctcaaaaatc tactcagtta cttatatttg aatttataga cggtacaatg  420

caacgctcat ggtctgcaag tgatagattt tctcaaataa agataccaac atatactacg  480

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cagaaatata ttccaaggga gagagattat gaggatccta ttgaggcaat gatgaaggcg  660
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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      260

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aagtccaaga aaagagagta ttttttcaat ccagagacga agcactcgca atgggaggag  180

cctgagggca ccaacaagga ccagctacac aagcacttaa gagaccatcc agtgcgtgta  240

agatgcctgc acattctcat caagcacaag gattcaagaa gacccgcatc gcatagatcc  300

gagaacatta cgatatccaa gcaagacgct acggacgaac tgaaaacctt aatcacgagg  360

ttggatgacg actctaagac gaactccttc gaggccctgg ctaaagagag atcagattgc  420

tcttcataca agcgaggcgg cgacctcggc tggttcggga gaggcgagat gcagcctagc    480

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<212>    DNA
<213>    Saccharomyces cerevisiae

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tcactcttgg agcccgtgac ccctccgcct ttgggccaga tgaataacaa aagaaaccat    180

caaaaggctc attcgcttga tctctctggt tttaatcagt tcatatcatc gacacaatct    240

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gatttcacgg ttgttgctcc ttcgaactct ggtgtcaata cctccagttt aattatggaa    480

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tctatggtcg aaatcagcgc actacccctt agagatctgg attatatcaa acttgccact    660

gaccagtttg gctgccgttt tcttcaaaaa aaattagaaa cccccagtga atccaatatg    720

gtgagagact tgatgtatga acaaattaag ccattttct tggaccttat tttggatccg     780

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ttaatacaaa caatatatcc aaatgttttc caaatatcaa tcaatcagta cggaactcgt    900

tccttacaga aaattataga cactgtcgat aacgaagttc aaatcgatct cattattaag    960

ggattttccc aagaatttac ttcgattgag caagtggtta ctttgataaa cgatcttaat   1020

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atagatgcta ttgtagaaca aaataatatc attaccattt ctacccataa acatggttgt   1140

tgcgtactac aaaaattact aagcgtttgt actctacaac aaattttcaa aatttctgtg   1200

302

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attaaaaaat tatttagaat cattactgga tttattgtta ataacaatgg gggtgcctcc 1440

caaaggactg cagttgcttc tgatgacgtg attaatgctt ctatgaacat tcttttgact 1500

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cctcgtatgc aatatcaaac ggaaggtgca aactgggatt caagtttgtc aatgaagtcg 2460

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<211>      1572
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      262

303

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cttcaaggcg catctaacgt gagtttaggg accactggta accaattgta catgggcgac   180

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gaacttttca ttaacagata tgcttctact tctcatgcca aaattgtgca cgaccaggtt   600

accgggatgt ctaagggcta cggttttgta aagtttacca attctgatga acaacagtta   660

gctctgtcag aaatgcaagg cgtattttta aatggtagag ccataaaagt aggacccaca   720

tctggtcagc agcagcatgt cagcggtaac aacgattaca accgtagttc ttcgtcacta   780

aacaacgaaa atgtagactc gagatttctt tccaagggtc aatcattttt aagcaatgga   840

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cagccgtctt taaaccactt cactgatccg aataacacca ctgtgtttat cggaggattg   960

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304

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<211> 2169
<212> DNA
<213> Saccharomyces cerevisiae

<400> 263

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aaccctgaaa ttacgagaaa ctttgatgac cgtcaagatt atttgttagc caatagtata     180

ggctctgatg taacagtaac tgttacttca ggtgtgaaat ataccggttt attagtatct     240

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ccaaaagaca tgctagaagt cttaaaaagg tcaagctcta cattaaaatc taattcttcg    1260

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305

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cataaatag                                                        2169


<210>    264
<211>    3402
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    264

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ttgaccgtgc gtgacgtaga gaatatcaaa cctagccata ttattaagag tccaacatgg  180

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307

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308

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309

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<213>      Saccharomyces cerevisiae

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310

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311

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312

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315

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<212>      DNA
<213>      Saccharomyces cerevisiae

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gataggacat gggcccatac taatagaaag gaacggttca gagaaatgac agctatcggg  180

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gcagaaacca gtgagtcttt tcctagggac ttgttaagta aatcaaatat tatcataaat  480

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316

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aatgatcact ttgaatcacc ctggcagaca ttttctttag ataagtatag gtttcaccga  960

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317

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<212>      DNA
<213>      Saccharomyces cerevisiae

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<212>    DNA
<213>    Saccharomyces cerevisiae

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319

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cccaaaagag caggcgaggc tgtcatacat ctaagtgagg ggagtaacct ttacccccgc 360

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320

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<211>      1632
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<213>      Saccharomyces cerevisiae

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321

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<210>      275
<211>      3117
<212>      DNA

322

<213>    Saccharomyces cerevisiae

<400>    275

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323

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324

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325

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326

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327

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328

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329

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330

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33

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<213>      Saccharomyces cerevisiae

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333

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      282

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tatgccatcg acttgccagc caatggtgcc tcagaggcgc cagcattgca agtgaacaaa   360

accaagaaga tcaagtctct caggtttaag catatagaag atgacgtagt aatccctgtg   420

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acaagaaagc tgaacgtacc gcggtttatc tttgaaaacc agctaaacgt tttgaagtgg   780

atgggaccca taggctccaa attgtgctcg aactacatct ccaccgcata cgtaaaagtt   840

ccggatcaga tatataagga ctatcttttg cactcatttg tcgggaagaa ccagacggtg   900

caaccacaga caatcaaggt gttcacccat ttgtttgaaa ggaatctgat cgctagagat   960

ccgataataa acaacgttcg tttttgaac ccagcaacgc ctgtcatgtt catgtatggc   1020

gagcacgatt ggatggataa atatgcgggc tacttgacta ctgaatcaat gctaaaaaac  1080

aaggcaaagg ctagctacgt tgaagtccct gatgctggcc ataatctttt cctggacaac  1140

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<211>      987
<212>      DNA
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334

<213>      Saccharomyces cerevisiae

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gcggctatag tttcataccc agaaaagaga aattcatcaa ctgcaaataa agaagatggt     180

aaattactgt gcaaggaaaa taaactagca ttgttactac acggaagtca atctcacaag     240

aacgctattt atcaaacttt actagcaaaa aggctggccg aattcggata ttgggtacta     300

agaatagatt ttaggggcca aggtgattcc tcagataact gcgaccctgg ccttggtagg     360

acgctcgctc aggatcttga agatttgagt acagtatacc aaacagtatc tgacaggtct     420

cttagggtgc aattgtacaa aactagtaca atatcactgg acgtggttgt ggcacattct     480

agaggatctc ttgccatgtt caaattctgt ctaaaattac atgcagctga atctccatta     540

ccgtctcacc tgatcaattg cgctggaaga tatgatggga gaggacttat tgaacgctgc     600

acacgactgc acccgcattg gcaagcagaa ggtgggtttt gggcgaatgg tccacgaaat     660

ggcgaataca aagactttg dataccatta agtgagactt atagtatcgc tggcgtttgc     720

gttccggaat ttgccacgat accacaaact tgttcagtaa tgtcctgcta tggcatgtgt     780

gatcacatag tgccaattag cgcagcctca aattatgcaa ggcttttcga gggcagacat     840

tcattgaaac ttattgaaaa tgcggaccac aattattatg gcattgaagg tgatcccaac     900

gcgctaggct taccgataag gaggggtaga gtcaactact caccactagt agttgatcta     960

attatggaat acctgcaaga tacatag                                         987


<210>      284
<211>      1368
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      284

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tggagaacgc aaccggtcaa agatttcgat gaaaaggtgg tggaagaagg ccccattgat     180

aagccaaaga caccggaaga tatatctgac aagccactac ctttattgtc tagcttcgaa     240

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tggtgtagta ttgatgtgga caacaaaaaa cagcttgaag atgttttcgt tctactaaat    300

gaaaactacg tggaagaccg cgatgcaggc ttcagattta actataccaa agaattcttc    360

aattgggctt taaagagtcc aggttggaag aaggattggc atattggtgt tcgcgttaaa    420

gaaacacaga aattagttgc ctttatctca gccataccag taacacttgg tgttagaggt    480

aaacaagtgc ctagtgtaga aatcaatttc ttgtgcgttc acaaacagct aagatcgaag    540

agattaacac ctgttctaat taaagaaatt acgagacgag tgaacaaatg tgacatctgg    600

catgcattgt acacggcagg tattgttttg ccagcacctg tgagtacgtg tcgttatact    660

catcgtccct tgaattggaa gaaactttat gaagtagatt tcacagggtt accagatggg    720

cacacagagg aggatatgat tgctgagaat gcgttaccgg ccaaaacaaa gacagcggga    780

ttgagaaaat taaagaagga agatattgac caagtttttg agttgttcaa aagatatcaa    840

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gaagaatcgt taccattgga taaacaagta attttctcat atgtagtcga acagcccgat    960

ggaaaaatta cagacttctt ctcattttac tcattgccat tcacaatcct aaataacaca   1020

aaatataagg acctaggcat cgggtacttg tattattatg ccaccgatgc agatttccaa   1080

ttcaaagaca ggtttgatcc aaaagctact aaggctttga aaacaagatt gtgtgaattg   1140

atttatgacg cttgtatttt ggccaaaaac gctaatatgg atgtttttaa cgcgttgact   1200

tcgcaagata atacattgtt cttggatgat ttgaagttcg ggcccggtga cgggttcttg   1260

aacttctatt tatttaatta tagagcaaag ccgattaccg gtggcttgaa tcccgacaat   1320

agtaacgaca ttaaaaggcg tagcaatgtc ggtgttgtta tgttgtag                1368
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gctttcactg acactgaaag attgattggt gatgctgcta agaatcaagc tgctatgaat    180

ccttcgaata ccgtttttcga cgctaagcgt ttgatcggta gaaacttcaa cgacccagaa   240
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336

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gtcttgggta agatgaagga aactgccgaa tcttacttgg gagccaaggt caatgacgct  420

gtcgtcactg tcccagctta cttcaacgat tctcaaagac aagctaccaa ggatgctggt  480

accattgctg gtttgaatgt cttgcgtatt attaacgaac ctaccgccgc tgccattgct  540

tacggtttgg acaagaaggg taaggaagaa cacgtcttga ttttcgactt gggtggtggt  600

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ggtgacaccc atttgggtgg tgaagatttt gacaacagat tggtcaacca cttcatccaa  720

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agaaccgctt gtgaaagagc caagagaact ttgtcttcct ccgctcaaac ttccgttgaa  840

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gaattgtgtg ctgacttgtt cagatctact ttggacccag ttgaaaaggt cttgagagat  960

gctaaattgg acaaatctca agtcgatgaa attgtcttgg tcggtggttc taccagaatt 1020

ccaaaggtcc aaaaattggt cactgactac ttcaacggta aggaaccaaa cagatctatc 1080

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gaaactgctg gtggtgtcat gaccaagttg attccaagaa actctaccat ttcaacaaag 1260

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gacaaggaca ccgtcaccaa gaaggctgaa gagactattt cttggttaga cagcaacacc 1740

actgccagca aggaagaatt cgatgacaag ttgaaggagt tgcaagacat tgccaaccca 1800

atcatgtcta agttgtacca agctggtggt gctccaggtg gcgctgcagg tggtgctcca 1860
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337

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gttgattaa                                                        1929


<210>    286
<211>    2067
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    286

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cagtacaatg caacggatcc cgtgagatta aagctttcc atacgcctcg gatggtttcg  180

caggggggctc attttgcatt ttgtttgccc actaagaaac cacattacaa gccattactg  240

ctttcgcaaa acgcacttga tgagtttaat ttggtgcagg atcaggactt ggagaaaata  300

ctatccggtg agaaagtata ttattccgat agtatctttc cctatagtac agtgtactcc  360

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gatcttaagg acaagtgtag cggacaatgg caaacgtttc agttgaaagg tgccggtatg  480

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ataatgagcg aggcgttgca cagtattgga attccatcca caagagctat gcaattaact  600

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tttgcgccca gctggatccg cttgggtaac ttcaacctat tcagatggcg gcacgacttg  720

aaagggttga tccaactatc agattattgc attgaggaat tgtttgctgg ggggacccaa  780

tttgagggga aacccgactt taatatattc aaaagggatt tttttcctga cactgagacg  840

aagattgatg agcaggtgga aaaggatgaa actgaggtga gtaccatgac cggagataac  900

atttccacat tgagcaaata tgatgagttt ttcagacatg tagttagctt gaatgcaaac  960

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gcccgtgacc ttgaattgtt acttaagggc gaactgaatt ctgttgatga cgccctagag 1260
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                                        338

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gaaaagtgca tgtcttctac aaacctcaaa gatatcgaac atgcagccga gaaggctaaa 1440

gagttctgcg atgttatcgt cgaaccattg ctagatattc tgcaggccac aaaagtcgac 1500

tataacaatt tttttatcca tctacaaaat tacaaggggc ccttcttcat caaagataaa 1560

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aagaaagcca acccgttgtt tgtccccaga agttgggtac tggaggaagt agtcgacgat 1860

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ctgcggccag aactggagac aaaatgggct gacctttccc accaagatga cgctaagttt 2040

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<210>      287
<211>      2643
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      287

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gggcacatcc ataactacaa caacctgacc tatatccatg gtcaccttca ccacagcgcg   180

cctgtgaacg acagtagtgc ttcggcaaca cctgcagccg cagctgttgc tgatgccgct   240

acttccgcat ttgcatctgg agctagccat gatatgggtg gtgattgcca cgtcaatgag   300

aaatgcaagg agtacaccga ctgccaacat ttcgagttct tgaattatca caataatccg   360

tcattaacaa aatataatga tactgcaacg tataattcta ataatcattc ttttgcaaac   420

aatttccatt cggtagcttc tgatccgaca agtccccaac agaattctaa aagcgaccta   480

ccacgtagaa aagattcttg gtttaacgac gatctgatac tgctgccctc ttccaagaaa   540
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339

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aagaacgatc acttgatgcc aaattttaac cttcatgatc agtactgtaa tagtaccaat  780

cacgactctc acaatcacaa taatactgta ccagatagct tttctcagct gatgtctcac  840

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aagattttgg aagatttatg caatatttct tctttgtatg aagtaccgtt tggaaaacac 1200

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aatgaaaacg gtaaccaaac aatgaatctt ctattatcaa gcattaatag atgcaaccct 1320

aaaaataatc ttaatggaag caataacaat acggctggag caacttcaac tgatcatcaa 1380

caccatcacc atagaataca gtttcattct cacaaaccaa atagaaacaa tattgtgaac 1440

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cagccggaac aggtgatttg ccaatgggat ggttgcaata agtcattttc cagtgctcag 2160
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340

gaattaaacg accatttaga agcagtacat ttaacccggg gtaagtctga ataccaatgc 2220

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gaaactttag ttcagcatac caggacacac tctggcgaaa aaccttacaa atgtcacatt 2400

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gaaaaacctt tacaatgcaa gatttgtggt aagagattca cgaatcgtc aaatttgagc 2520

aaacatatta agacccatca gaaaaaatac aagtgctctg actgttccaa aagctttgac 2580

gatttgggaa aattgaactc acagaaagtg aaatgcgcat tggaaagaaa accatattta 2640

taa                                                                2643


<210>       288
<211>       2748
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       288

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aagcttgccg aacccatagt gtttttaaaa ggatttgaaa ctaacggact gtctgaaata  180

gcccccagta tcttacgagg atctcttatc gtcagggtgt tgaaaccgaa taaattaaaa  240

agtatatcga taaccttcaa aggaatatcc agaacagagt ggccggaagg tataccaccg  300

aagagagaag aattttcaga tgttgaaact gttgtcaatc acacatggcc attttatcag  360

gcggatgacg gcatgaattc tttcacctta gaacatcaca gctcaaataa ttcgtccaat  420

cgcccatcta tgagcgatga agattatcta cttgaaaaaa gcggtgcttc agtatatatc  480

ccaccaaccg ctgaaccccc taaagataat agcaatctaa gtctggatgc ctatgagcgc  540

aactcattgt catccgataa tttgagtaac aagccagtat caagtgatgt tccccatgac  600

gacagtaaac tgttggctat tcaaaagaca ccattaccat catctagtcg aagaggatcg  660

gtaccggcaa attttcacgg taactctttg tcacctcata ccttcatatc tgatttgttc  720

acaaaaacat tcagtaatag tggcgctact ccaagtcctg agcaagagga taactatctt  780

acaccatcca agattctaa agaagttttt attttttcgac cgggcgatta tatttacact  840

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aatcagcatt tcaatgacat aaaccagatg ctaggcagta gtgacgaaga tgcctttccc 2460
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342

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tcagtcgata ttacagcatt ttatgatcca agaatgtcat cagattccaa atttgattgg 2640

gaggtaagca agaaccatgt tgacccagca gcctactcgg ttaacgttgc tagtgaaaac 2700

cgtgtactgg acgactttaa gaaagcattt cgcgaaaaga gaaaataa         2748


<210>      289
<211>      1854
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      289

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gaaagaagta ccccaaaaca ggaagataag gttacgggtg gtgatttttt cagacgtgct  180

ggaaggcaaa ctgggaacaa tggcgggttt tttggctttt ctaaggaaag aaatggaggg  240

acgagtgcga actataaccg cggaggcagc tcaaattaca aatcatctgg aaatagatgg  300

gtaaatggca agcatatacc ggggcctaag aacgcgaaat tagaagccga actgtttggt  360

gtacacgacg atcccgatta ccattcatct ggtataaagt ttgataatta cgataatatt  420

cccgtagatg catctggaaa agatgttcct gaacctatac tagattttag ttctccccct  480

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343

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<213>      Saccharomyces cerevisiae

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344

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346

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348

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349

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350

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351

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352

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<213>    Saccharomyces cerevisiae

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354

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356

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357

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358

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359

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362

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<213> Saccharomyces cerevisiae

<400> 302

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gctttttatg aagctggagg taattgtatt gatactgcaa acagttacca aaatgaagag   240

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<213> Saccharomyces cerevisiae

<400> 303

363

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ctactgaaga  aaacagagtc  ttctaaaagt  tttactaaag  gttattttgt  gttgactaca  1560

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364

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365

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gacggcgata atggtaagga tggtgacagc gaggggaaaa agccagctaa gaaggcaggc     360

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cagccgctag acgacccaaa cgtccaacaa gtgctccatc tcatgctcca ctatgccgtg     180

caagtcgccc ccatggctgt cataaaggaa atcgtccatc attgggtctc aactacaaac     240

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gctgacccct tcaagagaga ccgcaaggca aactgcccat cgagctcgtt aggaaagtca 720

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gatcttgttc tcttactcct tttttggcgt ccagataagc accccattg ggcttccgcc 180

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gaactctgtt atagcgaatc atccgataat ccctctagct cattgtttgt ctctaatttg 180

gataccaagg aaactttttt gaatgaagac aataatttgc agatttcttc cggactagac 240

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tcaaacgcaa aggctataaa cgcatacgga ggcattatca cgcaagggcc cgaggcaccc 360

atattagcta tgaaggtgtc cgactcaatg ccctatggag acggctccaa caaagttttt 420


367

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368

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<212>     DNA
<213>     Saccharomyces cerevisiae

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taccaaatat ccgcttacca acaagagca agacagaaag caagaacaga cgcacatacg  180

cctttggcac gcaattatat caaatcaatg gacctaatta gtaagaaaac caagacatca  240

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aaaaaactgg aaatcacatc cgacggagcg ctttcggtaa tgtgtgggtg cggtaccgtt   360

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ctactaaatt cttag                                                     435
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<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       311

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gaaaacaata ttgagtatct tttaactttt ttggctgaac aagccgcttt ctcccaagat   180

acaacagttg cagcattatc tgctgttctg tttagaaaat tagcattaaa agctcccccct  240

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gaggaagtta catatgacca cgctcgtcaa gctcttgatc gtgttgcttt aaagctgggt  1080

ggtgaatatt tggctgcacc attgttccaa tatttacagc aaatgatcac atcaaccgaa  1140
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372

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<212>      DNA
<213>      Saccharomyces cerevisiae

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ttagtttggg agagttggtt gacatattca attaaggaat catcgcttaa cgtagataga 180

aaagaccttg cattcaagcc gccggtcttt gctgttaaat gtgaatcatt gacactttgc 240

tggctaaggc aattgttttt atcaggtgtt tccctattta tagagtattc caaatcgctg 300

tccaataaat ctacaagacc accatgttca cccatcgctg gatatgccta g           351


<210>      313
<211>      1146
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      313

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gactctgctt ttaatgcagc ttactcacct catatgtatc cgaactctcc gtattatgaa 180

ggttcatgga ataccggtta tactcctcaa cttcatcatg tagcccctca taatcaatat 240


374

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aattacatac cgccagttca tcagaatata tcttatgcac cagcgcttaa tttacagaag   360

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tcaattagtt atgaagatgt tgcaataccg accgtaaagg aaatacaatt gattgagaaa   480

aacagaggga aagatacgtt tatgaatgaa ataagtccag taccatcaag caaggatcaa   540

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gaagatgatc ataataactt agggctagaa gatgatgatc gtgatgagca gttagaatca   660

gagggttgg gtaaggtggt tttggttcct ggaacctcca tagcattgat tactgatgaa   720

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agaggaaatc cgaagattga cttgaacttg aaattgatac agcgagaatt cgcaaacgaa   960

aactcccaac ttttggactt tataagagaa ttgggagatg taggattact tgaatatgag   1020

ctatctcaac aagaaaaaga tgtactttt gggagctctg aagataataa taaaaatcat   1080

tacaaaccaa attacaaaaa caggaaacct aatctgagta gagccaactt tactagaaat   1140

aagtaa                                                             1146


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<212>      DNA
<213>      Saccharomyces cerevisiae

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gctggagttt catatggtac ctttggttac tgtaaaactt tgaattcttt ttcctgctct   180

cgagtacgtt taatatataa cacctcgaaa gaaatattac ctggcccttc tcttgaacgt   240

tggtggctga gtcctaaggc aagacataca ataggaggac ttttgatttc gataccggtt   300

gctacatgtt tgactttcat ttcttttgca cttcccttgg ttattatttt tcttttttcag   360

actggaggaa ctaatgtctc acttattact tccaacgcta tattacacat attgacactt   420
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375

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acaatttcat ccttatacga cttggtgtgg ctggctaact gttccctgtt ccctctgctc    540

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      315

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aggtttaaag atgctactaa gatgtgtttt caccaccaaa tgctttcctc gagtgtcgaa    180

cctttcttct ctttgtattt caaccacgtt ccatatatgt ggtcgtgttt caactttttt    240

tcttcgtctc cttttcctcg ttgcaccaaa aattctccag aaaaaaagaa attcaaacgt    300

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<212>      DNA
<213>      Saccharomyces cerevisiae

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atcgacacgc agacgtccac gtttacgctc aagttccttc acacagaaac gggtcagaac    180

atcgagaaga ttatctactt cattgacaat gacacgggca cgatacccg cactgctacc    240

ggaatcaagc aaatcttcaa caagatgttc cgcatcgctg cggagaagag gaagctgtcg    300

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<400> 317

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tccagactag atttgtatct gacaagaagg aggctggata cgtccatcaa tttacctaca 180

aacaccaaga ccaaggacca tccccccaat aaagagatgc tgaggattta cgtctacaac 240

actacggaaa gcagccctcg cagcgattct ggcaccccag cggactcagg caagactaca 300

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aagaagagga aacgcgattc gtcattgagc cttcctttga tctgcaaca acccgaatac 480

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ggaagactat aa                                                    1452


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<211>    2157
<212>    DNA
<213>    Saccharomyces cerevisiae

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tctattatcc atgaattcga cccctggttc aattataggg ctaccaaata tctcgtcaac   180

aattcgtttt acaagttttt gaactggttt gacgaccgta cctggtaccc cctcggaagg   240

gttactggag ggactttata tcctggtttg atgacgacta gtgcgttcat ctggcacgcc   300

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tacttctaca tggtgtcggc ttggggtgga tacgtgttca tcaccaactt gatcccactc   660

catgtctttt tgctgatttt gatgggcaga tattcgtcca aactgtattc tgcctacacc   720

acttggtacg ctattggaac tgttgcatcc atgcagatcc catttgtcgg tttcctacct   780

atcaggtcta acgaccacat ggccgcattg ggtgttttcg gtttgattca gattgtcgcc   840

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gagataaaag agcgtgattt ctataccgca gagggagaat acagagtaga tgcaagggct   1860

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ccaccattag actacttcga cgaagttttt acttccgaaa actggatggt tagaatatat   2040

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<210>      319
<211>      3660
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      319

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ctgacgcttc tttctaaaat ctccgacgaa gccataaatg aaaacttgaa gaagagattt    180

ttgaatgcta caatctacac ttatataggt catgtgttaa ttagtgtcaa tccattccga    240

gacctcggaa tctatactga tgctgttatg aatgaataca aaggtaagaa tagattggaa    300
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gaaaatcagt gtgttattat ttcaggtgaa tcaggtgccg gtaaaactga agcagctaaa   420

agaattatgc aatatattgc ggctgcttct agcacacata cggagtcaat tggaaagatt   480

aaagacatgg ttttagccac taatccattg ttggaatctt ttggctgtgc aaagactcta   540

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tgcatatctg ctgagacaat tgatgatttg caagattatc aagagacatt aaaagctatg   840

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acctcagtaa ccgattttgt tgcttacttg ttacaaatag atagccaatt gctgattaaa  1020

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gttccattga atattgtcca agcagatgcg gttagagatg ctttggcaaa ggctatttac  1140

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gctgaaaaat ccattggtat tcttgatatt tacggctttg aaattttga acataactct  1260

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tactttgata caaggttgt gtgtgatttg attgaggcaa gaagaccacc tggtatattt  1440

gcagcaatga atgattctgt tgcaactgca cacgcggatt caaatgctgc tgatcaggct  1500

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aataaggatc aattacaaaa ggatctggta gaattaattg gtaccactac caatacattt  1680

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tcatatatca gaacaattaa accaaacgaa accaaatctc ctaacgatta tgacgatcgg  1860

caagttctac accagattaa gtatctaggt ctgcaagaaa acgtgcgtat cagaagagca  1920
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gattatggta cgaaggtttt gggtggaaga aaagaaagaa ggtctatgtc cttattaggt 2340

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catacaaaat ttggccgttc tgcacaaaga ttgaaaaaaa ctttcctatt aactccaact 2520

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gccattaagt tggctagctc aggtcaacct gaccccttaa tcaacacata tttcaaaaca 2700

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cctaaacccg ttctgaattc tgtacaacat gataacacct ctgcaaacgt tattccagct 3540
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381

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<210>      320
<211>      1746
<212>      DNA
<213>      Saccharomyces cerevisiae

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aacttaattg agggcgaaga gcaagagggt agtgaagaag aaccttccta taccggcaat  180

gacgatgaga cggagaggga aggtgaatac cattcgttgt tagatgccaa caattcgcgg  240

acattgcaac aagaagcgtg gcaacaaggt tatgactctc acgaccgtaa gcggttgctt  300

gacgaagaac gggacctgct aatagacaac aaactgctct ctcaacacgg caacggtggg  360

ggagatatag aaagtcacgg acatggccaa gcaattggac cggacgagga agaaagacca  420

gctgagattg caaatacgtg ggagagcgcg atcgagagtg gtcagaaaat cagcacaact  480

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gctattcccg gcgtggtgat ggtggaggca gagttcctcg ctttgaagt gttgacaatt  1260

382

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tttatcggcg cgtcgctata cgacagctgc atgatcacgt gccgcgtgtc cttattgttg 1440

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gggagacaaa aaaataggtg ggtacatcaa cctagtcgca ttctactgcc taggtgtgcc 1680

catggcatat gtgttagcat tcctgtatca tctgggtgta ggcggcttat ggttgggtat 1740

aactag                                                                1746


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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      321

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ctctgtgcat ccgctgctca tcggctctct gaaaccttcc ctatgcgttt ggtagtcgcg   180

cgtgaatatg ctaattgggg cgccttccaa catgcgttta cgcggcgcgc tggagcttct   240

gtggcggcga cttctgcatg gtttgatgca gttgcggctg gtactgaaaa tgcacatatg   300

cagtcagctg aatcatgcaa ttaa                                          324


<210>      322
<211>      2280
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      322

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tctaggagtt cttctgcagc caatgtacgc tccggaacag gtgcaaatac acttactaat   180

ggcggcagta ctagaaagag acttgcgtgc actaattgta gaaatagaag gaaaaaatgt   240
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383

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gatttaggat ttccctgtgg taactgttcc aggttggaat tggtttgtaa tgttaatgac 300

gaggacttaa gaaagaagcg gtacactaat aaatatgtca agtctttgga gagccatatt 360

gctcaactgg agaccaactt aaaaaaccta gttcagaaga tctaccctga cgatgagcaa 420

atactgaacc gaatgatggt aggtgatgta ttatcagctc taccagacag ttcacaagtc 480

tcaatcaatt atactgacca aactccctct cttccaattc ccgcaaccag aggtacattc 540

attattgaaa acgataaggt cagtcaacct ctatcgtcct ttaaccaaca aacagagcca 600

tctactctaa actcgggtat cttcaacacc caaaaacaaa atttcgaaga atcccttgat 660

gatcagttac ttttacgaag atcgttaaca ccgcaaggtg aaaaaaagaa gaaaccgttg 720

gtaaaaggta gtctttatcc tgaaggacct gtcagttaca aacggaagca ccccgtaaaa 780

tcggacagtt tattgcctgt gtcttcgtta acagctgcta cagacccatc tactttttct 840

gacggtataa ctgctggtaa ttccgtccta gttaatggtg aactgaaaaa acgtatatcc 900

gacttgaaga ccaccgtaat agtaagagga ctaaacgatg ataatcccaa ctctatcaat 960

aacgatccca ggattttaaa atctctttcc aatttctata agtggctgta tccaggttat 1020

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aggcttacac cggatctaca agaatattca gaagtgtatt atcaacgaag taagaagact 1200

ttattacagc tcgtctttga tgagcaaagt acagcccgta tcaccaccgt ccaagcgcta 1260

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ggcctggcta tcagggtcgg ctacgacatg ggatttcaac tggaccctaa agtctggtac 1380

gttgatgata acaatctgca gctgacccaa agtgagttgg aaataagatc aaggatttac 1440

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gcacgaaaac taaagtactt gaacactttc aattctcagg tttacaactg gagacaatct 1740

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cccactatat cttacttctg gtattgctac tacatagtgc ggctcacctt taacaagcca 1860
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384

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ctttactcat gcctgttggc catcaactgt ttgaagaagt tgaaagagat acgttccagt 2040

gagcaagact catggaatgc acaattggat tttttcaatc acatcttcta cacacaacta 2100

tatcccgcat atgatctgcc gaaaaagctg caggaggata cggagctgga aacagaacaa 2160

gaaaaccaga tgttgaacca agttggaaat ataaactaca cgcacgattt ttcactctcc 2220

cacgaaattg acgatcttat cagagaactg tttggggtgg cacacctca aaaactctga 2280


<210>      323
<211>      1023
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      323

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cgtaatccag atgaacaaag tggctttgtt aatccacctt tgtataaggg gtcaaccatc     120

attcttaaaa aacttagtga tttagaacaa aggaaaggaa gattttacgg gacagcaggt     180

tctccaacta ttgacaattt agaaaatgcc tggacgcatt taaccggcgg tgctgggaca     240

gtgctatcag cttctgggct tggttctatc tctttggcgc tattggccct ttcgaaagct     300

ggtgatcata tcttgatgac tgatagtgtc tacgtgccaa cacgtatgct atgtgatggt     360

ttattggcca agttcggtgt tgaaacggat tattatgacc catcaatagg gaaggatata     420

gaaaaactag ttaagccaaa tacaaccgtc attttcctcg aaagcccggg ttctgggacc     480

atggaagtac aggatattcc agctttggtc tctgttgcca aaaagcatgg gataaagaca     540

attctagaca cacatgggc aacgccactc ttttttgatg ctcatgcgca tggtatcgat     600

atttcggtag aagctgggac aaaatatttg ggtggtcatt cagatcttct tattggtctg     660

gcctccgcaa atgaagaatg ttggccgcta ttacggtcaa cttatgatgc aatggcaatg     720

ttaccaggtg ccgaggactg tcaattagca ttgcgaggaa tgcgtacatt gcacttaaga     780

ttgaaagagg tagaaagaaa agccctggat ttggctgctt ggctcggaaa tcgagatgag     840

gttgaaaaag tgcttcaccc cgcctttgaa gattgtcccg acatgaata ctgggttcgt     900

gactacaaag gttcttcagg cttatttttcc attgtcctta aaaatgggtt cacaagagct     960

385

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ggtctggaga aaatggtaga agggatgaaa gttttgcaat tgggatttttc atggggtggc  1020

tag                                                                  1023


<210>      324
<211>      336
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      324

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aatctacggg aaagaagaaa tttttttaaac ttaatgcaaa ataagctttt ttcttggaaa  120

ataagatttt cggcaataaa aggtaaatgc agccaaaaat caaaatactt cagaagaagt  180

cgtagcgagg actgctacgt ggaagcggat ttgaagatcc tttccagaac aagaaggagc  240

cgaaagctgc caggaactgt cctgatttt ttaggaaaac aattaatagg tatctcgtct  300

agcgtagtat ctcgagtttc cagaagttgc agataa                            336


<210>      325
<211>      2589
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      325

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acacaagcac ttctacaaaa cccaggggac gattttccat ttagcacagt aatagatatc  120

ctctcagaaa atgttgaatt ctcaactttt ttaaggatta ttcagaaaac tggtcacgta  180

cagtacttaa atgagctaca gaactttaca ctttttgctc cgattaattc agcatttatt  240

aaggggggacc aaaccacaga ccaatttgag gagcatttcc atattgaaga tttccttatt  300

catgataggg tattgcaagt gagagacctt gaaaacggta cctacctgga gaaaagagct  360

gcaaaagcac ctttattgct gagaaagcat gagcgccatt gctttgtcaa tgaaattgct  420

gttgtcgaac ccgatttgct gcctagtttc cagaatgctt cattacaagg tattaacaat  480

cttttactaa ttcaacctca aataaatgag ttgctggtac aactagatga agaaacccaa  540

gattaaaga tatttagtga ttttatcagc agttttttcaa actataatgc atatacaaac  600

tcatccacag ttttagtgcc cttagatgtt aatttttcgaa aattcttcaa tacaatcgaa  660
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386

ataaactatc tacttgacaa atataataaa ttgggtaaat ctaatacaat ttctcaggcc 720

aaatgggccg cagatagaac ttcccttctt caagaactca ttattgatga cgtgtatggt 780

ggtattttac ccaaggaact aattttagaa aataaaaaca atcgaaaact ttttatgaag 840

agtaattcag aaggtacatc agtaagtgta aataattcag attactcacc catatcaaac 900

agaattttg aaataggcgt cgtgcatgga ttttctgact tagacttttt acgaacgcat 960

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gtagaaggta aaattgacct tgaacaggac ttttcctcat tgcgcccgat tcaatacgca 1200

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caattaccgg gcgacttagt gttgtcatta gcaccagaaa accactgttc tatttcccta 1440

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cttcttccat gtatgaattc atgggacaat aatgatttga ctatagacta tttgaggtca 1560

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ggaacaaaag aaatatttga cttttttaac ttgttttatg acctttcttc aatcatttgg 1920

aataacgaag agtactcgct tttagttcca acggcttctt ctattccatt aagtggcatc 1980

acggcgaact cgacaaactt aagaaaattc ctcgaactcc atttgattcc tgctaatgta 2040

acgcaaaacc tactagactg caatggctcc attagcacta aactaggtac aaaactaaac 2100

tgcagaaaag atcatctgga caacgttttt gttagcatac agggcgactg gaccaaggaa 2160

gttagagttc ttaaaacagg atgcactact aatttgaaaa gttcatgcat atttctgatc 2220

gacaaaccca tatccttatc ttggctaaac agcgagaaat accatctgcg cttgccaggg 2280

387

atagcggttg  gatttggggt  tataataggt  gttaccatag  ccatttcttt  attgttttgc  2340

ataataatta  ccaggggtgg  aaaagtaaaa  gacaaaaatc  aaagagggag  aaatgatcga  2400

gcaacaacac  cactgattca  acactctccg  ataatccaca  acccttctta  ctcggcaaca  2460

gcgcatttat  caccactttc  tcaacccact  tttgaaggtt  catattctgt  gaacgctata  2520

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acctcataa                                                              2589


<210>      326
<211>      2250
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      326

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ggggatttaa  aagtggtgaa  ggacgtggtc  gaaagtggag  cagtggatat  taataacgac  240

cgcattgatg  aattatccgg  cttacactgg  gcctgtataa  acaataggtt  ttctgtagca  300

aagttcctat  tacttagggg  agcaaatcct  aaccaggcgg  caggccccgg  aggggctact  360

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ggcgctgatc  cgacgctcaa  agatgagcag  ggtcttaaca  tcatgcattt  tagcgtttac  480

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ggagattttc  tcactgtaga  actttttattg  aaatttggct  ccacagttgc  atggacggac  660

aacagagggt  tcaatgctct  ccattgtgct  ctagttggag  gtgatcaaag  ggtcatatgt  720

gacttaatac  ttagcggtgc  aaatttctac  gaaaggaata  accagaagca  agactgtttt  780

gatctagccg  aaggaatggg  aaccaaatca  cttttgaac   aagcgttgca  acatcatgga  840

tatgacaggc  ttggaaatca  gaaagacaaa  ctgttcaaga  aaagctcgca  tgcacaattc  900

acaatttttt  tgtcaccatt  tttactcatg  gtttacatat  acttaatttc  tctcgttctt  960

tctccagtgc  tagccattat  gctttcccta  ctggtcactg  ttgtcatggt  caacacatta  1020


388

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actcccttttt tcagtggcct ctttctgtcc actttctgtt ttttaatata tatatggacg 1140

aagaaactct atccatatag tgtatctgac tataccatga aaaacgtcca gtttttggtt 1200

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ccaagtgcga ccaccattac tcacacaatt tctattgatg gtttggaacc aagaaatagg 1920

cgccgcgcca ttcttagcgc ttgcttttca atgatgggta ttaatcaatg gctcgttact 1980

attaaggaaa tagtaggtat aacccacatt ttgcatggac aggttccaca acaacatcac 2040

agttcattgc ttcgaagttt cttagtgaca aatcactgga agacgaattt gacggatttt 2100

tggcttaata gtgatgtaac agcgcccttg tggcaacgat ttttctattc ttcggatact 2160

tcaaaagcta tgttgggtgg aactgaggtt gactactacg agctatacga atatccggcc 2220

cgagaaggag aagtattacg tccaaactaa                                     2250


<210>        327
<211>        375
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        327

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cccacaatca acgaggtttt ctcatttgaa ttactggaac tagaactaga ggaggaggaa   120
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389

gataaactac tcagttgtga atcggactgt ttcgcacagt atgtggatgg gcacttgtca    180

catgttaatg aagtcataac acaatattct cctgaagcgc aaacagggca tgatgcagtt    240

gaatcgcaaa caacacatcc gtcgctgcct ctagttgcag aagttgaaga ggtggctgtg    300

cttgacaagg atgaacttgc agaagccttg gaggagctcg acattttttg tttgattttc    360

agaaaacgaa cgtaa                                                     375


<210>       328
<211>       921
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       328

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aataatgaag aatacataat actctttggc ggaggtcggg acctgatact aggctccctg    180

acaccttgtt cgagctctca tttgtccaat caagccaacc cacaagacac cagtgagtat    240

ggcacagacc tgtttatact caacagctgc attatcattt ggttcaatgg cttgggatat    300

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390

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tgggacagtg tttttttat caagaacata acttccaaaa acggaaaacc tcaatttgag   240

catgaatacg cgttttctca gttgtggact tttttcgtta ggctgtttat taaaagtaat   300

aacgatagca tctaccatgc cttaagggtt ggagttgcaa tagaaaatgt tttattttac   360

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agatattggt ttccttactc ctttatcagc atggcttgct ttaccttagc atccttgaat   660

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ttacagacta tcctatttgc agctttttta ccaccagcct ga                     1302
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tatgtaattt atatgataaa aacttttcag ctcatcgaga aaaattttct ttcctcccac   360

gcaggatag                                                           369


<210>       331
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tacgatttca aaatgaacca gcagctggct gagatgcagc agataagaaa caccgtctac   180

gaactggaac taactcacag gaaaatgaag gacgcgtacg aagaagagat caagcacttg   240

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caacagcaac agcagcaaca ggtccagcag catttacaac agcaacagca gcagctagcc   360

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ccccaggttt ccgtggcacc attgagtaac acagccatca cggatctcc tacttctaaa   660

gagaccacta ctttaccctc tgtcaaggca cctgaatcta cgttgaaaga aactgaaccg   720

gaaaataata ataacctcgaa gataaatgac accggatccg ccaccacggc caccactacc   780

accgcaactg aaactgaaat caaacctaag gaggaagacg ccaccccggc tagtttgcac   840

caggatcact acttagtccc ttataatcaa agagcaaacc actctaaacc tatcccacct   900

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tccggcaatc cgttattgat gttgcaaggt cataggaatt cagttatatc tgtggctgtg 2040

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<210>      332
<211>      3108
<212>      DNA
<213>      Saccharomyces cerevisiae

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393

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gctccagggt tttcgctgcc atacttcatt aactctttga aaaccgtctc tcatgatggt   360

aagtttcttt tgaatgttgg tgctttaaac tacgacaatg ctaccggctc tgtcaccaac   420

gattatgtaa ccgcattgga tgctgcttcc aagctgaagt atggtgtcgt gactccgatt   480

tccgctaacg aggtacaaag tgtcgcctta ctggcattgg cgattgccac tttcagtaat   540

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394

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aaactaagac ccgatttacc cgtcaagaac ttcgtcgtga aagttaaaga aaatagacgt 1980

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<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    333

395

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396

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taa                                                                  1923


<210>    334
<211>    447
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    334

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acttacgttt ctggtttaga attgacacgt aaagtctacg aaagaaaacc cactgaaaca   180

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<210>    335
<211>    2667
<212>    DNA
<213>    Saccharomyces cerevisiae

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gttggcgaca tcagtaggga tgacaacata caaatttact ggagggatcc tacattattt   180

gcacaatata taactgattc taatgtggtc gctcaagaac aagccattgt tgccttgaat   240

agtttaatag atgcctttgc gtcatcgtct ttgaaaaatg cacataatat tactttaata   300


397

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398

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<211>      3591
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      336

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406

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410

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411

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412

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413

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414

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415

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418

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419

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aaccccattt atggactgga gttgaagtct accattccag tgaaaaggga tggtggtgta   420

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422

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424

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425

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426

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<213>      Saccharomyces cerevisiae

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436

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gccatcggtg accaggatac tttttaccaa tgtttgtcag gaaacttcta caacttatac   960

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aacactgcta ctgccccagt cccagaagtg caagaacaag agagctccaa gagcaagcaa   180

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<212>      DNA
<213>      Saccharomyces cerevisiae

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aaaagattgg ttgcagtcaa atacattttc aaattagaag atgacggcca gtacgatggg   180

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<211>    2043
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    361

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gcacacgttc tatggagtca aatgcgcatg aacccaacca acccagactg gatcaacaga  180

gatagatttg tcttgtctaa cggtcacgcg gtcgctttgt tgtattctat gctacatttg  240

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ccaactttga tcaaaatgac cacaaccatt ggttacggtt ccttgcatgc cggctctcac  780
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taa                                                                 2043


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<211>      1572
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      362

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aagaaggaaa acgtccatgt tgagaaaggg cacgattggt ctcaactcag tacgagcaga  360

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ccattacaaa agacgaagta tttcccaaca aatgagaatc aaaataccga tatagaaaat  480

cagaattggt cccaaatccc caatgaagac atatgtgcac ttatagagaa gattgctagc  540

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443

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tgggagggca gaatttacat atctgaatga                                   1770
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<212>      DNA
<213>      Saccharomyces cerevisiae

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445

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446

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ccactagact tggatgatga cgaagacgac gacgaatttt acgatgatca atctaatatt  660

gaagataata ctgctttgct gcatcattcg cagtataaca ttaagtctca gaaaaaatcg  720

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447

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acaatggtca gtgtgtccaa gacctccccg cgttgtatca gagtgctaaa atctgccctt    360

actgtaatta tttcagaaga ttaccctagc aaaaaatggg gcaatttgtt accaaattcc    420

ttagaattac tcgcaaatga agacatcaca gtaacatatg tcggacttct gtgtcttgct    480

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ttcgtttcat accatgacct accatttaca ttacaacgct cagaatcgtt taccccatgg    720

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449

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450

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<212>      DNA
<213>      Saccharomyces cerevisiae

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aaggaataca atgataaagt tgcttctatg ccacgtgttc cattgaagat tgtcttgaag  240

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451

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<211> 2007
<212> DNA
<213> Saccharomyces cerevisiae

<400> 370

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caacagaaga atcgacgtca attgaaacac atctgcatga aatcaagaaa agagtatttt   180

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453

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gaatcgccgc taaatttcaa ggatgatgat acgcatgaag gcagaaaaaa tacctccaat 1920

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<212>      DNA
<213>      Saccharomyces cerevisiae

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gggaaaataa acagccttac ccaacggtca tcaatgggga agggagattc attaaattct   300

cctttaacga aggaaccgca gcacaaaact aggtctcaca atagaacttc gagtctccct   360

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caccaaagaa taagctatga tgaggctcaa cgtacgttca aggattttgg cggaccacag   480

gccagaggaa ttttaacggg acaacaccgt actgaaaatc ctagcgggtc tattcctttg   540

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gccttgaatg caagaaatgg ttcactttta agaaaaaaag tatcgcagga atctttacat   720
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454

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458

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466

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469

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471

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472

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tgtgacgaca agatcatgta cgttgactac aagaacatca ccaaggtcat ctccgctggt  420

agaatcatct acgttgatga tggtgttttg tctttccaag ttttggaagt cgttgacgac  480

aagactttga aggtcaaggc tttgaacgcc ggtaagatct gttcccacaa gggtgtcaac  540

ttaccaggta ccgatgtcga tttgccagct ttgtctgaaa aggacaagga agatttgaga  600
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473

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attgaaaacc aacaaggtgt taacaacttc gacgaaatct tgaaggtcac tgacggtgtt 780

atggttgcca gaggtgactt gggtattgaa atcccagccc cagaagtctt ggctgtccaa 840

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aacttcggta ttgaaaaggc taaggaattc ggtatcttga agaagggtga cacttacgtt 1440

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taa                                                                1503


<210>      384
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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      384

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acggaagtgc ggtcattcta cgaagacgaa aagtctggcc taatcaaagt ggtaaaattc 180

agaactggtg caatggatag gaaaaggtct tttgaaaaag ttgtcatttc cgtcatggtc 240

gggaaaaatg taaaaaagtt cctgacgttt gttgaagacg aaccagattt ccagggcgga 300

ccaatccctt caaacaaacc acgtgatggt ctacacgttg tttcaagtgc atactttgaa 360

attcaatag                                                          369


474

<210> 385
<211> 1875
<212> DNA
<213> Saccharomyces cerevisiae

<400> 385

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agtgacaggt gcagaaagta ttgcagcagt gatgaggaca gcgacacgtg cattcatggt   240

agtgctaatg ccagtaccaa tgcgactacc aactccagca ctaatgctac taccactgcc   300

agcatcaacg tcaggactag tgcgactacc actgccagca tcaacgtcag gactagtgcg   360

actaccactg aaagtaccaa ctccaacact aatgctacta ccactgaaag taccaactcc   420

agcactaatg ctactaccac tgccagcatc aacgtcagga ctagtgcgac taccactgaa   480

agtaccaact ccaacactag tgctactacc accgaaagta ccgactccaa cactagtgct   540

actaccaccg aaagtaccga ctccaacact agtgctacta ccactgctag caccaactcc   600

agcactaatg ccactaccac tgctagcacc aactccagca ctaatgccac taccactgaa   660

agtaccaacg ctagtgccaa ggaggacgcc aataaagatg caatgctga ggataataga   720

ttccatccag tcaccgacat taacaaagag tcgtataagc ggaaagggag tcaaatggtt   780

ttgctagaga aaagaaact gaaagcacaa tttcccaata cttccgagaa tatgaatgtc   840

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atatacttct gcccagaggg agtattcaca caatacggat tatgcaaggg ctgtcaaaag   960

atgttcgagc tctgtgtctg ttgggctggc cagaaagtat cgtatcggag gatggcttgg  1020

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gacatcgagc catatcatgg gaccctgta gggtatttga aatttttag cgtaaaaagg  1140

ggagagatct actctcagat acagagaaat tatgcttggt acctggccat tactagaaga  1200

agagaaacaa ttagtgtatt ggattcgaca agaggcaagc aagggagcca agttttccgc  1260

atgtctggaa ggcagatcaa agagttgtat tataaagtat ggagcaactt gcgtgaatcg  1320

aagacagagg tgctgcagta ctttttgaac tgggacgaaa aaagtgccg ggaagaatgg  1380
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475

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aggcatcatc gacagttgag gagcagatat gaattaagtc taggaatgca cttgcgagat 1560

cagcttgcgc tgggagttac cccatctaaa gtgccgcatt ggacggcatt cctgtcgatg 1620

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gcagataaca cgagggtacc gctgtacatg ctgatggtag cggttcacaa agagctggat 1800

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gaagttggag agtga                                                   1875


<210>      386
<211>      1785
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      386

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aatgccgatt tcattttcaa tgaacaagaa atggatgttg aagaccagga ggatgaggga  180

tctgaatcag ataacagtga agaagatgaa gcgcagaacg gtgaattaga ccatgttaac  240

aacgatcagt tatttttgt ggacgatggt ggtaacgaag atagtcaaga taagaatgaa  300

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aataagacaa agaaattaag aacctcctat aacgagtcca aaatcaacgg tgttcattac  480

atcaacagat tgagatctca gtttgaaaag atatatccaa ggcccaaatg ggtggacgat  540

gaatctgatt ctgaattaga tgacgaagaa gacgatgaag aagaaggctc taataatgtt  600

attaatggag atattaatgc tctaacgaag atcctgtcta ctacttacaa ttataaagac  660

actttatcga attccaaact attacccct aagaaacttg acattgtgcg tcttaaagat  720

gcaaatgcat cacacccgtc tcattccgcc atacaatctc tttcattcca tccttctaag  780

cctctactgt taacgggtgg gtatgataag accttaagaa tatatcatat tgacgggaaa  840


476

acgaaccatc tagtgacaag tttgcacctg gttgggtctc caatacaaac atgtactttc    900

tatacttctc tatcaaacca aaatcaacaa aatatattca ccgccggtag aagaagatat    960

atgcattcct gggacttatc cttagaaaat ttaactcatt cacagactgc caaaatcgaa   1020

aaattttcca gattgtatgg acatgagtcc actcaaagat catttgagaa tttcaaagtt   1080

gcacatttgc agaattcaca aacaaattct gtccatggaa ttgtcctttt acagggtaat   1140

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gaaggtgtga taacggattt ctgtatcgat tatcaaccta tttcacgtgg taagtttagg   1260

accattttaa ttgctgtaaa cgcgtatggt gaagtgtggg aatttgactt gaataagaat   1320

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ggtggtggga caacaactac ttgtccggct cttcaaataa gtaagataaa gcaaatagg   1440

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ttgagactag ttcatctgcc ttcttgtagc gtgttcagca actggcctac cagcgggacg   1680

cctttgggta aagttaccag tgtcgcattt tcgccatctg gtgggctact ggccgtgggt   1740

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<210>    387
<211>    411
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    387

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aaagaggata actatcctct attgaatgaa acagcggcat ggccagatgg ggtgattacc    180

tctgaagaag gatgttcatc ttcaggtgag aaagagaatt caggcttatg ttcagaagaa    240

agttcagaag aagatccaga agaagctgaa gaggaatctg caagggcttt tggagagtta    300

gttgcagtct tgcgggacaa agacatacca ctgaatgtat tggacgaacc tcagatgaaa    360

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477

<210> 388
<211> 2433
<212> DNA
<213> Saccharomyces cerevisiae

<400> 388

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agtttagctg ctgattctcg gaatgctaat ttctcgtatc acgagaatca gcagttgttg  240

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gaaactagcg tttccaaaag aaacccacac agggattttt ataatgttag gaaagtggac 1080

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atcggtgaat ctcgtctcag agaaattttt ttgaagacaa acaactacat caagggtacc 1380
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478

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tgggtgattg acaacaaagt tatttcccat aatgttcgtt ggttagtcca aattccgagg 1560

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gaagaatact cagttgcagc acaaatttat aaattgtcta atgtagatat gtgtgaattg 2220

gcaagaaatt ccgtgttgca aagtgggtgg gaagcacaaa tcaaaaaaca ttggataggg 2280

aaagattttg acaagagtgg tgttgaaggt aacgatgtgg ttagaacaaa tgttcctgat 2340

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<210>    389
<211>    2589
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    389

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tgttctccct ttcatgtgag gttcggcaaa tttcaaattc taaagccatc tcaaaagaaa  180

gtccaagtgt ttataaatga gaaactgagt aatatgccaa tgaaactgag tgattctgga  240

gaagcctatt tcgttttcga gatgggtgac caggtcactg atgtccctga cgaattgctt  300
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gtgtcgcccg tgatgagcgc cacatcaagc cccctcaat cacctgaaac atccatctta 360

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gtgctagagg aaccagattt tttagatatc aatgacactg gagattcagg cagtaaaaat 480

agtgaaacta cagggtcgct ttctcctact gaatcctcta caacgacacc accagattca 540

gttgaagaga ggaagcttgt tgagcagcgt acaaagaact ttcagcaaaa actaaacaaa 600

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gaacagaatg gcagcaaact accaaatggg cctgtgattt tatcacccga tagaacgatg 1440

gctgcgttaa ggcgggaagt aatactaaaa aaacctgaag tctttaaaat cgcgtgtcta 1500

aacgacataa gatccttgta ttttgaagac agtgataacg aagtggatac agaggaaaaa 1560

tcaacaccat tttttgccgg ctttggtaat aggattactg atgctttatc ttacagaact 1620

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480

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<210>       390
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<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       390

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tctttcagta ctacaaagcc gaccgaatat aacttaccaa aagaacagcc cgaatcaacg    180

tccaagaatt tggaaaccaa ggctaaaaac attctgttac cttggaggaa gaagcataat    240

aaagactcgg aaactccaca cgaagacact gaggcggacg ctaaccgccg tgccaacgta    300

acttctgatg tgaaccctgt ttctgccgac accaagtcaa gttctggccc taatgctact    360

attactaccc atggatactc ttatgtcaaa caacgacac ccgctgctac aagtgagcaa    420

tccaaagtga aaacgtcacc tcccactagc catgaacatt caaatataaa ggcgtccccc    480

actgcgcata gacattccaa aggtgatgca gggcatccaa gtattgcaac cactcataac    540

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cctaaatcca ccgctgctgc acaggatcat tccagtacta aaactaaccc ttcagttact  840

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gttgttatac cttctagtat gaaggagaaa ttcgacagcg gtacatctgg atctcagaat 1560

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tcaaatgcaa agaaaaacga cttgtattct aagaaagcgt accagggaaa accatcggat 1920

tacaattatg agcagagaga gaaaatccca ggtacttttg aacctgatac gttgtcaaaa 1980

tcagtgcaaa acaagatga  agacccgttg tctccaaggc aaaccactaa ccgtgctggt 2040

atggagactg caagagatga gagtcttggc aattacgaat actcgaatac ttctggtaac 2100

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gatttcacca ataatccgga aacaggtact actggaaacg tagatacaac cggaaggatg 2280
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482

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483

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484

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<213>     Saccharomyces cerevisiae

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gagcaaatta gaccttttgc taccgctgct gtattgagaa atatcaagct taacgaaaaa  360

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487

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488

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489

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490

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491

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492

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495

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496

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agtagcaatg aaattgccaa tcatgaaccg gttttttgaaa aaattcctgt acagtgcgac   480

aatccattac agaatctaat cttatcggaa gacttgacat tagttgcgga tcttaattat   540

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497

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<213>      Saccharomyces cerevisiae

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498

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499

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500

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508

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gattacaaga gacctaccaa atttcaggac aagtattata tcccggtgga tcagtatcct     480

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gatgtcaatt ttgttggttt attattaggt cctcgtggac gtacgttaag aaagctgcaa    540

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gcaagtgact tacctccagg cgccatgaac tttgaggacc ccttgcactg tttaattatc    660

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gcggtgacat ctccggaagg ccagaatgac ttgaaacgag acaactgag agaattggcg    780

gaacttaatg gtactttaag agaagataac aggccctgtc caatctgtgg tttaaaagat    840

cataaaaggt acgattgtcc aaacagaaaa atcccaaata tacagggcat tgtttgcaaa    900

atatgtggac aaactggaca tttcagtaga gactgtaact catcgtctca aagaatgagc    960

cgttttgaca gaaacgccac ggtaaataat tctgcgccaa tacagagcaa tgacgtacac   1020

tataatagca atactcatcc aattcaagca ccaaaaagat ctcgttatga caataactcg   1080

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gcgtcacata tttcgaggca agctcaaaac gtgacgccta caccccctcc cggcctaaca   1200

tcaagtagct ttagttccgg agttccagga atcgcccctc ccccattaca aagccctcca   1260

gagtcggaac aaccgaaatt ttcgctacct ccacctcccg gtatgactac ggtacaatcc   1320

tcaattgcac ctcctcctgg cctaagcggt cctccagggt tttctaataa catgggcaat   1380

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<212>      DNA
<213>      Saccharomyces cerevisiae

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gtagggaaga gctcatccag gggtgccatg gatcaaaaat ctgatggaac ctttagactt    180

aagtctatct acaggcatgg cgtcggagca aaccatcggc tacaccagag gctggaggtc    240

actccagaag ttatttctgc cgctggaatg ctgtatcaag aaaccacaac tcaaggacag    300

gatttcgaag accaagaacc cctatggact a<:taatgccg aatatgccac cactaaccca    360

ttcgattttg agtttgagct acgaaggatg c<:gctattga tgaagcggat gaaggaaaga    420
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511

gatcctgaat tcatagagtc gtacatttac ggagaaacat acatgacgga ggaggaagaa 480

cacgccatgt ggatagatga tgacattgtg gcacccaata tcacagatag aggtacagta 540

gtgtcgttag cattaatgtc gtctaatgct tacgtgagaa taccgcaaac gggagactgg 600

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atgtggtcaa cgacaagggc tggagtgtaa 1290


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<212> DNA
<213> Saccharomyces cerevisiae

<400> 414

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tcaggcgatg ctaagatggc tattttttgac gagctcttac agatgccaga aacaaagctt 180

gttgcaggtg gtgctgctca aaacactgct agaggggcag catacgtttt gggcgccggc 240

caggtggtgt acttcggttc cgtcggtaag gacaagttca gcgagagatt gcttaacgaa 300

aacgaaaaag ctggtgtcaa gtctatgtac caagttcaaa atgatattgg taccggtaag 360

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512

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tacatcggtg gtttccactt gaccgtgtct ccagacgcta tcgttaagtt gggccaacat    540

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gaggccgaag cctttttgcga cgccttccaa ttagactgtg ccaacactga tttggaagct    720

attgctcaaa gaattgtcaa ggactctcca gttgaaaaga ctgtcatctt cacccacggt    780

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gactcttcta agatcgtcga caccaacggt gctggtgacg ccttcgctgg tggctttatg    900

gctgggttga ctaaaggtga agatttggaa acctctattg acatgggtca atggctagct    960

gctttgtcta ttcaagaagt tggtccctct tacccttccg aaaaaatatc ttactctaaa   1020

tag                                                                  1023
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ctaaaaatta ataatcctgc aattgatacg gtaacattga acaccgtcga taccgacatc    180

cattctgcaa aaatcggtga tgtcacatct tccgagatta tctctgaaga ggagcaacaa    240

gtcaccacat ttgcgtttcc taaagggacc atgtcttctt caagggtaa tgcattтттg    300

gatataaaat ttactggtat tttaaatgat aatatggctg cttttacag agccaaatat    360

gaggacaagt taacaggtga gacaaaatac atggctacta ctcagatgga acctactgat    420

gctagaaggg ccttcccatg ttttgatgag cctaacttga aagcctcttt tgctattact    480

ttagtttcag acccatcttt gacacaccta tccaatatgg acgtcaagaa cgaatacgta    540

aaggatggaa aaaaggtcac tttgttcaat acgacccta aaatgtcaac ttaccttgtt    600

gctttтattg ttgctgaatt gaagtacgtt gaatccaaga actttcgtat tcctgtcaga    660

gtttacgcca ccccaggtaa cgaaaaacat ggtcagtttg ccgcggattt gactgccaag    720

actttggcat tttттgaaaa aactттtggc atccaatatc ctctacctaa aatggacaat    780
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513

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gaggtagttc aacatgaatt agctcaccaa tggtttggta acttagttac tatggactgg  960

tgggaaggct tatggctaaa tgaaggtttt gctacttgga tgtcatggta ttcatgtaat 1020

gagtttcaac cagaatggaa agtttgggaa cagtatgtta ctgatacctt acaacatgca 1080

ttaagccttg actctttaag gtcctctcat ccgatcgaag tacctgtaaa aaaagctgac 1140

gaaattaacc aaatctttga tgccatctct tactcaaagg gtgcttcttt attaaggatg 1200

atttcgaaat ggttaggtga agaaactttt attaaaggtg tatcccaata cctgaataaa 1260

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aatggagttg acagttccgt tgtattgagt gaaagaagca aaactattga attagaagat 1560

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gaaaaattag ccgcattaag atctttaggc agatttaaag aacctaaatt attagaaaga 2220

accttaggat atttgtttga tggcactgtc ttaaaccaag acatttatat tccaatgcaa 2280

ggaatgagag ctcatcaaga aggtgtagag gctttgtgga attgggttaa aaagaactgg 2340

gacgaactcg taaagagact acctcctggt ctttcaatgc taggctccgt cgtcacatta 2400
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514

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gcgcagtggg gttaa                                                  2535


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<212>    DNA
<213>    Saccharomyces cerevisiae

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aagcaggtag atttgtccac tgaagtgcaa tttgtgtccg atttattgat tgatgcgggt   180

gcgtcaaagg ctaaagttaa agaactatcg aaagtatttt gaagcaatt gactactcaa    240

ctaaaggaga acgaagccaa attggaattg accggtgata cgtccaagag attacttgat   300

attaatgtct taaagagtca taacagtaaa tccgatatca acgtctcatt aagcatgctg   360

ggtgtgaacg gtgacatcga acatactggt agaaagatgg aaacaagagt tgatttgaaa   420

aaactggcca aggctgaaca aaagatcgca aagaaagtcg ccaagagaaa taacaaattt   480

gttaaatacg aggcttctaa attgatcaat gaccaaaagg aggaggatta cgattctttc   540

tttttgcaaa tcaacccttt agaattcggt tcatccgctg gtaaatccaa ggatatccat   600

attgacactt cgacttgta cgttggtgac ggtcaaagaa ttttgtccaa cgcccaattg    660

actctaagtt ttggtcacag atatggtctt gtgggccaaa atggtattgg taaatctact   720

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gtggaacaag agttaagagg tgatgataca aaggctttac aaagtgtgct ggatgcagac   840

gtttggagaa acaactatt aagtgaagaa gccaagatca atgaaagatt aaaggaaatg    900

gatgtattaa acaggaatt cgaagaagac agtttagaag ttaaaaaatt ggacaatgaa    960

agagaagact tggataacca tttgatacag atttctgaca aattagtcga tatggaatct   1020

gacaaggctg aagctagggc agcatcaatc ttatatggtt tggggttcag tacggaggca   1080

cagcaacaac ccactaattc cttttccggt ggttggagaa tgagattgtc cttggcaaga   1140

gccttattct gtcaaccaga tcttttgttg ttagatgaac cttccaatat gttggatgtg   1200


515

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tctcacgacc gtgcattctt gaatgaagtg gctacagata tcatttatca acacaacgaa 1320

agactagact attacagagg ccaagatttc gatacctttt acaccacaaa ggaggaacgt 1380

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<212>    DNA
<213>    Saccharomyces cerevisiae

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atgccactga cagctgtcaa gccaaggtgt ttgctgccac tggctaacgt acctctcatt   180

gaatacacct tagaattttt ggctaaggct ggcgtacatg aagtttctt aatttgctct   240

tctcatgcca accaaattaa tgactatatt gagaattcta gtggaactt gccttggtct   300

516

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ccatttaaaa ttaccaccat tatgtctcca gaagctagat gtacgggtga tgttatgaga   360

gatctagata atagaggtat cattactgga gattttattt tagtcagtgg tgatgtattg   420

actaacatcg atttcagcaa aatgctagaa tttcacaaaa aaatgcattt gcaagataaa   480

gatcacatct cgacaatgtg tttgagcaaa gcgagtacct atccaaaaac aagaactatt   540

gagcctgccg catttgtctt agacaaatcc accagtaggt gtatttatta ccaagattta   600

ccattaccaa gctctagaga gaagacttcc attcagattg acccagaatt gttggataat   660

gtcgatgaat ttgtcataag gaatgacctc atcgattgta gaattgacat ttgtacatct   720

catgtacctt tgatatttca agaaaatttt gactaccaat cattaaggac agactttgtt   780

aaaggtgtca tttcaagcga tatattggga aagcatatat atgcctattt gacggacgaa   840

tatgctgtaa gagttgaaag ttggcaaact tacgacacca tttctcaaga ctttttaggt   900

agatggtgtt atcccttggt cttagactct aacatacagg acgatcaaac gtattcttat   960

gaatcaagac atatatacaa ggaaaaagac gttgttttgg cccaatcctg taaaattggt  1020

aagtgcactg caattggatc aggaacaaaa atcggagagg gtacgaaaat tgagaattcc  1080

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acactagccg tttctattgt tggagataag ggtgttggtt atatttacga aagcgaggtg  1440

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ttagatgagt tatacttaag tgacgattca atttcttccg ccactaaaaa gacaaagaaa  1560

agaagaacga tgtctgtcaa tagtatatac acggatagag aagaaattga ttctgaattt  1620

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gcaactcaaa cattaggtcc caaggacgct gtggtgaagg tttttaatca gtggggactg  1860

ttgttcaaga gacaagcctt tgatgaagaa gagtatattg atttgatgaa catcataatg  1920
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517

gaaaaaattg tagaacagag ttttgacaaa ccggatttga ttctatttag tgcattggtt 1980

tctctatacg ataatgacat aattgaggag gatgtcattt ataaatggtg ggataatgtt 2040

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<212>      DNA
<213>      Saccharomyces cerevisiae

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ataagatttt cggcaataaa aggtaaatgc agccaaaaat caaatactt cagaagaagt  180

cgtagcgagg actgctacgt ggaagcggat ttgaagatcc tttccagaac aagaaggagc  240

cgaaagctgc caggaactgt tcctgatttt ttaggaaaac aattaatagg tatctcgtct  300

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<212>      DNA
<213>      Saccharomyces cerevisiae

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tccaaatttc ttgggaaaat tgaagaagag gaagaagagg aggaagaagg caaggatgag  300

gaaagcgtgg attctcgtat taaaaggtgg tctccgttcc atgaaaatga aagtgttact  360

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aaccagcgat ggtttccgaa aaatgatgct cgcactgaaa atacatcctc atcctcttca  480

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aacaagttca aaaaaatcaa aagagcaagg aattcggtta ttttgaaaaa tagagagcta  960

acaaacagtt tacaacaatt caaagatgat ttatacggca cggacgagaa tttcccacct 1020

ccaatcataa tatcaagtca tcattcaact agaaagaacc ctcaacctta tcaatttcgt 1080

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attggggcaa catctcaaac acatagagaa agcagaccat tgtcactctc ctctgccatc 1200

gtgacaaaca caacaagtgc agagacgcat tccatatctt ccaccgattc ttcgccgtta 1260

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gcaccagaaa tcatttctga ttgtacgtac gattacaagg cagatatttt ttccctgggt 1920

ctgatgattg ttgaaattgc agcgaacgtt gtgttacctg acaatggcaa cgcatggcat 1980

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aagaatcgtc ttattttgca taaaagttct aaaattcccg catgggtacc gaaatttctt 2280

attgatggtg aatcacttga gagaatagta cgatggatga tagagcccaa ttatgagaga 2340

aggcccacgg caaatcaaat cttacaaact gaggaatgcc tgtatgtaga aatgacacgc 2400

aatgcaggtg ctattatcca ggaagacgac tttggaccta agccaaaatt ttttatatga 2460


<210>      420
<211>      1668
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      420

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ttaatcttcg ttggtgctac cattggtggg cttttattcg ctatgatac tggtgttata   180

tcaggtgttc tgctttcttt aaagcccgaa gatctatctt ggtagttttt aacggatgtt   240

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agaatgctat atcctactgc atctacatat catgtgaata gtaaaattaa gcagctgata   780

attgaactcg ataagttacg actatacgaa gatgcaagtg aacctttact agtacagtcc   840

caatcggtta ttcgatacat ggatagttca acctcaggaa ctcttagccc acctaacatt   900

aaaagacttt cctcgaacac agaaagaact agcaacacaa tgtcctcctc atcagcatat   960

ctatcggcgt tgcgaggccc agctccaaac ggtgccctgg catctaacaa aaagaaaaga  1020

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520

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ccatggacct gtgtggaatt tctccccttg aacaggagat catttggggc atcatgtata   1440

gcctgcacaa attggttgac caatgcattt gtttcaatga catatctgag cactattaac   1500

accattggtg atgaaaatac aatgctcatt tttgcttttt tcacagtttg tgcctggttt   1560

ttcgtatatt tttggtatcc agaagtcaaa ggtttgtcac tggaagaggt tggaagggtt   1620

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<210>      421
<211>      2493
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      421

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aactacgagg ttagttcact attttatggg acggaacggt ttcagattca aaaccatttc    180

caatcgctcc tagatttagt agaccttaat aatgaaaatg gtggcttggt attcgacttg    240

ataataatga gtgcgtcttc actgcaagaa atcccgcagg tattgagaga tataaaacct    300

atgatgaata agacaacaaa gatactattt gaaagtagcg ggtttatata tttggagcca    360

ttcatcaagg cttcagttga tctttcgctg tcaaatattt tcagcatttt caccgattat    420

gacataagac ggttggacaa tggctcatac aaacagttca cgactgcaaa tgccaaatcc    480

ttttctgttt cgatcggtca aacgacatcc gttcacgaaa acagctattc aagtgatatt    540

attcctattt tgaatacatt tcagaaattg ttccaaaaac tgtttcctag ggacgttgtg    600

actctttacg atcattctcc ctccgctttc ttggcaaaag aatgggaact agctttgcct    660

caaatatgtt tcgatccatt attaataata ttagaagaga agaatccatc aaccttggat    720

gaccacgttt tggccaaacc tcttatttca ggtttactag gcgagagctt attaataata    780
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521

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cataaggctt catctttgaa tattgactta ttgttattac agccgatatt attagcagat  960

gactttggcg tgaagacacc atatttagaa tgtttgttta caatgatgac tcaatatcaa 1020

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cgcgttgatg atttacaaaa cagtatcgca cttaaagatg gaaaaatcat gcagctgcaa 1140

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gaacttcaag agcgtgagtt agagttacag agaaaagccc tccagcaaca acaacaatat 1560

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tcaaaccaaa gtacgtttag atctcaacag ggtccaccga taacacagca aaaatcgttt 2040

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atcaatatta cgcaaccatc accaattcag accaactttg ctacgagtga taaccctgct 2340

gctgtaataa aactagggac accttctgaa gatacagttt cagctgcggc aacagccaat 2400
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522

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aagttcagtt tctttggaaa aaggaaaaag taa                               2493


<210>    422
<211>    1731
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    422

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cacccagcac cacctcatga ggcaaagcgt ccacaccatg gaaaaggtcc catgcactca  180

cccaaatgtg agaagattga accattaagt ccatcattca acattccgt cgacacaatt   240

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tcctggaagt ccctccatt ttctggtcac tatgatccag aaacagattt tgtttggggg   600

cgtggttcta acgattgtaa gaacttgtta attgccgagt ttgaagctat cgaacaactg  660

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ggccatggtg gtcattcctc tgtcccacct gatcatacca aatcggtat cgcttcagaa   960

ctgattactg aatttgaagc caacccattt gactacgaat ttgagtttga caatccaatc 1020

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acaattttgg gcgcaccatt ctgtcctaga aggaaggaca agcttgttga gtacatttcc 1140

aaccaatcac atttgcgcag cttaataaga acaacacaag ctgttgatat catcaatggt 1200

ggtgttaaag ctaatgctct gcccgaaact accagattct tgatcaatca cagaattaat 1260
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523

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gagaagtatg gctatggttt atctaagaac ggtgacgatt acattatccc tgaaaccgag 1380

ttaggtcaca ttgacattac tctcttgaga gaattggaac cagcaccact ttcgccaagt 1440

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aaatactact ggaatttgtc caagaacatt tataggtttg ttggctctat cattgatatt 1620

gatttactga agacattgca ttcggttaat gaacacgtgg atgtcccagg tcatttatct 1680

gccattgcct ttgtttacga gtatatcgtt aatgttaacg aatacgctta a        1731


<210>      423
<211>      2199
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      423

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tatttggtgg aaagggcctc agacactggt gacgatgata acgagcacga tgtttccccc  180

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gaattcttcg aaagtcccta cgaggggggac ttgattagtt ggaatgtaga cgtaggagat  300

gaagtagcca ctgctaacca agtgatttgc gaaataaaaa ggccatgtaa ccatgacatc  360

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gtaccactag acgttgtcgg ggacgtggat ttacagatta gcgagacaga agccattaga  480

acaggcaagg cattgaagga gcatttgcga cgggataaga aacttatctt agtggtggat  540

ttagatcaaa ccatcatcca ttgtggcgtg accctacga ttgcagagtg aagaacgac  600

cccaataatc cgaattttga aacattaaga gacgtcaaga gctttacgtt ggatgaggag  660

ttagtactcc cacttatgta catgaatgac gatggttcta tgctgagacc gcctcccgta  720

agaaaatgtt ggtactacgt gaaggtaagg cccggtttaa aggaattttt cgctaaagtg  780

gcgcctcttt ttgaaatgca tatctacaca atggctacaa gggcttatgc cttgcaaatt  840

gccaaaatcg tggaccctac gggcgaattg tttggcgata gaattctgtc gcgtgatgaa  900


524

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aatgggtctc taacaactaa atcattagct aaactttccc ccactgacca gtcaatggtt    960

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ccttataact tcttcgttgg tgtaggtgac attaattcta atttcttgcc caaacaatct   1080

acaggaatgc tacaactagg gaggaagaca agacagaaga gccaagaatc tcaggaactg   1140

ctgacggata ttatggataa cgaaaaaaaa ctacaagaaa agatagataa agaagttaaa   1200

cgccaagaag aaaaattgaa ccatcaactg gcgactgctg aggagcctcc tgcgaacgaa   1260

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gcgaaaaagt tcaacccaca gattaaaatt gttcacccag attggatatt tgagtgtttg   1740

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gacgaggaat tacaaaactt caaacacaa ttacaaaaaa gacaagaata tctggaggag    1860

acccaggaac aacagcatat gttgacatca caagaaaatc taaatttatt cgctgctggt   1920

acttcatggt taaacaatga cgacgatgaa gatattccgg acacagctag cgacgacgac   1980

gaagatgacg accacgacga cgaaagtgat gacgaaaaca actcggaagg cattgacaga   2040

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tctcaagatg gtcctgtaca acataaagga gaaggggatg acaacgaaga cagcgattcg   2160

cagttggagg aagagttgat ggatatgctg gatgattag                          2199


<210>      424
<211>      936
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      424

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525

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atccagccgg tacagacccc cgttactgta tgtggagaca tacacggcca atttcatgac  180

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ggtgattacg tggatcgtgg ctactatagt ctggaaactt ttacgctttt aatgtgtctg  300

aaagtcaagt acccggcaaa gataactttg gtcagaggaa accatgagtc cagacaaatt  360

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gacaatgtag aggcttggca agtttcccct cgtggtgcag gatggctctt tggcagtaaa  660

gttgctagag agtttaacca cgttaatgga ctgaacctta ttgcccgggc tcaccaactg  720

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<210>      425
<211>      3405
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      425

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aacggtgccg gccaatatgg tccttctcaa cacccagcat attacaccaa ctcaccatta  180

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tattatagaa tggggagaaa ttctttctcg aggaacaaca acagtacgag gaatgttact  480

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cacaacaaca ataaggggtg cgacacccgg aacaacagtg gaagaagaac attcgcaagg  540

aataacattt tcgacgacat acttccagaa atgcttttac aaagacccct ttgtattaat  600

tacaaggttc taccgactgg tgatgatgct tatagaacta ggtcgctgct tattgaaaat  660

gtggatcatt ctattgattt acactctata gtcaaaaatt ttgtcaaatc caatactctg  720

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acagaaaacg ctgaagaagc cgacattacc aatggttcaa caatgatcag tgcttcgctg 1020

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aacaataata aaagtaatat gagtggtatc accacactca ataataatag tagtattggt 1500

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caaagggtgt tgccgaatcc aataactcaa agtttggagc aaaatttcaa cgtttcggcc 1920

aaagtggcat catccatggg ttcagacata ggcaatagaa caatttatat aggaaacatt 1980

aatccaagat caaaggcgga ggatatctgt aatgtcgtgc gtggaggaat ccttcagagc 2040

attaagtaca taccggagaa gaagatatgc tttgttactt tcatcgaagc tccatccgct 2100
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527

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cagctcaatt ataggtcgtc attaagacaa gctcctccaa gagctccctc aactttgtca 3180

tataatcact cgaagaacaa cgaaacgcca atgcaagata ttttcacaaa tggcgaaaca 3240

gcaaataaca gaaagaagaa gagaggatct tttgcaaggc atagaacgat accaggatct 3300

gacgtcatgg cccaatacct tgcacaagtg caacattcga catttatgta tgcagccaat 3360

attttgggcg cctctgcgga agacaacacg catcctgacg agtag         3405


<210>      426
<211>      345
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      426

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aaggaaatcg actcatacaa aattcaaaaa gacaaggaat tgaaggagtt tgaacaaaag     180

aatgccggtg gtgttggtga attggaaaag aaagcagagg ctggtgtgca aggtgaatta     240

gctgagatta agaaaattgc agagaagaaa aaggatgacg ttgtcaaaat tttgatcgag     300

actgtcatca agccttctgc tgaagtccat atcaatgcct tgtaa                     345


<210>        427
<211>        2841
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        427

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gattccaccg aatcactaat tcatggaggc gcagaaaggt atattgttaa cgctttaaag     180

cctatagaat aaataaaaac tgaaggcttt ttcgaagacc cgccgttcca tcttccttct     240

ccaccggttg attcgacaaa tctggagtat gaagacgtta ccgatcttcc taagaatggt     300

ttacgatatg atttgaatga tatatccgtt gaggtaatcg aagatttata ccgccagatt     360

gaagcttttt tggttcattt caaactatcc agaagttttt tacaaatttt caaaaactat     420

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gaagatgaac tgaaaggttt tttcacttttc aattctgtta tagaagagat tttagaaata     540

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530

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531

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532

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536

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537

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538

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545

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547

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548

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ggccttcttg aagtttctat ttcaagatca tcaaagatga ctaaccaagc atttttaacg     240

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cttaaagcaa ggaaacttaa acgcaagtta cgtagtgatg atatatgcgc caaaaagttc     480

aggcttaaaa ggcaaataag acgcctgaag cataagctga atcaagaaa ggtagaggag     540

gctgagattg ataggattgt aaaagaattt gaaacccgta gattggaaaa catgaagtct     600

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atggaaaatc caccgaacaa agtccttctt atacaaaatt tgccaagcgg cactaccgag     720

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<213>      Saccharomyces cerevisiae

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aagtccaaga tggacaaacg cagagattta ttgaaaagag ggtttcttac attgggtgcg  480

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550

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<213>      Saccharomyces cerevisiae

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ggggataacg ttgagccacc aaaaagaggg ctcataggtt atcttgtcat ttacttactg  180

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tgtccaatgc ttttgtctga aatagccccc acagatttga gaggtggact ggtctcattg    600

taccaactga acatgacgtt cggtattttc ttgggttatt gtagcgttta tggtacgaga    660

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actaccattt ttaaatcagt cggtcttact gatgggtttg agacgtcgat cgtcctaggt   1080

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<213>    Saccharomyces cerevisiae

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aaaacttcta ccgaacaaga actgattaca agtatgagcc ttagtcagag aaaccatggt  240

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cctaacgatt ctgagacaac tctcaaggat agtaaaatgc atgaatatac tatgacaaat  480

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aagatcaatg aaaaagtcgg aaaatataaa tcttgtttag aaactcttca agaaaggatt  720

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caccaactat atcagagaag gataagcgga tttaagacaa gtattgaaaa cttgaacaaa  840

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aaaatcaaaa acagttcctt aatacaggaa atgggaaaaa atagagaaga aatgattaaa 1020

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553

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<213>      Saccharomyces cerevisiae

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554

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cagtattatg attccaaact tttcgaatgt atgaagtcac attttggaag ggaattttcc   660

acccttgtaa gcgctactat tcatcactat attcatatgt ttccaataac gaatacaatg   720

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555

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<212>      DNA
<213>      Saccharomyces cerevisiae

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ccagcagatt tcgttccaga ttccgtctct ggaatgttca gaagccatga ctttagttat  360

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560

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gatatgagta acctgcttaa tgttcatcaa acaacactg atcttcctca taatatcata    240

gaaccatctg attatggtga ctatgtgaaa aaaccacgtg ttgttctgaa tgaaaggaag    300

cgcaggcgaa gaagagcaac cgtgttgcaa ccagcttccc attctgggag ttgtacagtt    360

tcgagtcaag attcctccag tgtacaaaac aatgggaatt taagcgctcc gttggcgtca    420

aatgacgccg ggaacgctgg tgtaagtaca ccattggtgc attgccacgg agcaatatca    480

cgtagcggat ccaatcattc tgactgtgca agaaatagtg cagattatca aatgttgcaa    540

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cagcatgttg caaacgaggc tattcatagg aattttatga caagaggat taggccggat    660

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aaatttccga aaagcccgtc ttcatctatt gtggtttttc cttcctcggt agctagttca   1320

561

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acggaagtgc ggtcattcta cgaagacgaa aagtctggcc taatcaaagt ggtaaaattc   180

agaactggtg caatggatag gaaaaggtct tttgaaaaaa ttgtcatttc cgtcatggtc   240

gggaaaaatg tacaaaagtt cctgacgttt gttgaagacg aaccagattt ccagggcgga   300

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<213> Saccharomyces cerevisiae

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caagagatca cacctaccac gacaaaggaa gcccaagaaa gcgcatcaac tgtagtttct   180

accggaaaaa gcttagtaca aactagcaac gtcgtcagca acacctatgc tgtggctcca   240

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gagacgtcaa gcggaatcac caactccgca tcctcctcaa cgacatcaac atcaacggac   420

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accactacgt caggttctac agtagagaca ctgaccacta catacaagtc tacagtcaac   660

562

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563

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564

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aatggtagca actatcccca aagaagcct tacaacagca acagacctca tcagcaaaga   180

ggtggtaaat ttggaccaaa cagatataac aaccgtggca actataatgg tggcggtagt  240
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565

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566

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cgcacgtcgg aacggtcctt agccgctagt gtaaaggacg gaagttgctc aaatagcaaa      180

agcaataagc ggaactcttc ggcatccgtg tcaggggaag aagataaatc ctgtctaatt      240

tcacttaatt gcctatgttg tggtgtccca ctacggtttc cagcctccat aacgaaattt      300

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568

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gcattttgtc tgtatgattc caagaaagac cgtattgtcg ctgcaagaga ccctatcggt  420

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gaattaaaat gtctaactga cgtttgtgac agtatcattt cgttccctcc tggtcatgtc  540

tacgattctg aaacggacaa gattactcgt tactttaccc cagactggtt ggatgaaaag  600

cgtatcccat ccaccccagt tgactaccat gctatcagac acagtttaga aaaggccgtt  660


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<213>    Saccharomyces cerevisiae

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tttctattca atataaatca aaggtttta atattgaacc tgatagtgga ttttcctatc  300

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aatgactcat cttccatatc gaataacgta tactcgtctg agtaccatcc aatcaaacct  720

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<213>      Saccharomyces cerevisiae

<400>      457

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ttcacccaaa atcaattacg caaccatcaa actaagggta attcagaagg attcaaaggc   660

caccctatgt gtgccttctg ttccggaaaa cgattttatt cagacgacga attgtacatt   720

cacatgagaa atcagcatga aaagtgccat atttgtgata agatgaaccc cgcttctcct   780

caatacttta aggattataa tcagcttttt gaccacttta aacattcgca ttacgtttgc   840

accgtccaaa cttgcttaga taacaagttt gtcgtattta agacgagtt ggagttacaa   900

gcccacattt tgcaggagca tggtaatatc ctgaagggaa agccaaagtt tttccagtca   960

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ctgaaaagtc cttcagcgtc gtatgatccc tttgcaacca ccgtaaaaaa aaacactctg  1560

agacccgtgc aaaacattaa aagaactaca cctcaatcag ttagttatcg aacttccact  1620
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572

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<212>      DNA
<213>      Saccharomyces cerevisiae

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<213>        Saccharomyces cerevisiae

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575

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577

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583

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gatgctatcc aaattataac gagtcatggg agaatgaccg acatgtttgg taacaaagac 1980

ggaggtgggt tcgctgaatt gcagccacct aatggccaat atatcctagg tgtgactggc 2040

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<212>        DNA
<213>        Saccharomyces cerevisiae

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gaattggagc aggagacaaa aaaattaagt gaggaatcga agagatactc gactgcggtg  180

aatggaatgc tgacacacca aattggattt gccaaatcca tggaggaaat tttcaaacct  240

atcagtggta aaatgagtga ccctaacgct accataccag aggacaaccc acaaggtatt  300

gaagcaagtg aacagtatag ggcaattgtc gcagaattac aggaaacatt gaaaccggat  360

ctggctttgg tggaagaaaa aattgttacg ccatgccagg aactgttgaa gattattact  420

tatattcgta aaatggccac caagagaaat cacaaaaaat tagatttaga tagacatcta  480

aacacttata acaagcatga aaagaagaag gaaccaaccg ccaaagacga agaaagattg  540
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585

tataaagcac aagctcaagt ggaagtggct caacaagaat atgattacta taacgacttg    600

ctaaagactc aattaccaat actgttcagt ttggaagctg aatttgtgaa accattattt    660

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ggcaatgtgg aagaacaaac ggacgccttg actattacac actttaaact cggttactct    840

aaggcaaaat tggagatgac cagaaggaag tatggtgtag caaccgccga aggctcaccc    900

gtcagtggcg catcaagcgg tgtcggatat ggtgctgggt atgatccagc aactgccact    960

tctccaaccc ctacaggata cggttatggt gccgcagcac caagttacgc cgctcaacct    1020

gctgcccagt atggtactgc tgccgccgtt ggtactgctg ctgctgttgg tactgctgct    1080

ggtgctgctg ctggcgctgt tccgggtact tatccacagt atgctgctgc gcaatctcca    1140

ccgctcactg ggctaggctt ccaacaatca ccacagcagc aacagggacc accaccggcc    1200

tactctaatc tctaacatc acctgttgcg ggcacaccag ccgcggccgt agcggcagct    1260

cctggcgttg aaactgttac cgcattgtat gactaccaag ctcaagctgc tggtgatttg    1320

tctttccctg ccggcgcagt tatagaaatt gtccagcgta ctccggacgt gaacgaatgg    1380

tggacaggaa gatacaatgg ccagcaaggt gtgtttcctg ggaactacgt gcaactcaac    1440

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<213>       Saccharomyces cerevisiae

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gatgaagtaa agcctgtgcg tacaaagaac agaagaccca agaggatgc attcactcaa    180

caaagattag cggctataaa cccggtgtta acgccgagga cagttttgcc tctttatctg    240

ttaattgctg ttgtatttgt tattgtagga gggtgcatat tagcacagaa ctccaaagtg    300

gatgaagtaa ccatatatta ccaggactgt atgactaacg caacctcatc atggagcgac    360

atcccttctg aacattggca atttgtattt cacaaatata aacatataa tactgcacca    420


586

caatggaggt ttgtggatga tgaatcagat gacttcacaa aacaaagagg tacatgccaa    480

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aaatttgctg ccaatcacag aagatatgta ctatctttta gcgaagatca gatacgtggg    600

gaggacgcct cttatgagac ggtgcatgat gcaaccggta taaattgtaa gccactatct    660

aagaacgccg atggtaaaat atactatcca tgtggcctaa ttgcgaactc aatgttcaac    720

gacacgttcc ccctgcagtt aacaaatgta ggggatacgt ctaacaacta ttcattgaca    780

aataaaggaa tcaattggga atctgataaa aaaaggtaca aaaaaaccaa atacaattat    840

acacagatag cacctccacc atattgggaa aagatgtatc cagatggata caacgagacg    900

aatattcctg atattcagga ttgggaagag ttccaaaact ggatgaggcc aggtgctttt    960

gataaaatta caaaactgat cagaatcaat aaaaacgata ctttgccagc gggtgaatac    1020

cagttggata tcggtctgca ttggccagta ttggagttta atggtaagaa gggaatctac    1080

ttgactcacg gttctcacct tggcggtaga aatccatttt taggtatagt ttacctgatt    1140

ggaggctgta tttgtgctgc catggcattg atattattaa cgttttggct cttcggcggt    1200

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<210>      470
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<212>      DNA
<213>      Saccharomyces cerevisiae

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tccttcttcg atgggcctcc atttgccacc ggtactcctc attacggtca tattcttgct    180

tccactatta aggatattgt tccaagatac gctaccatga caggccacca cgtggaaaga    240

agattcggtt gggatacaca cggtgttcca attgaacata tcattgacaa gaaattaggt    300

atcacgggta agatgacgt cttcaagtat ggtcttgaaa actacaacaa tgagtgtaga    360

tccattgtta tgacttatgc cagtgattgg agaaaaacta ttggtcgttt gggtcgttgg    420

attgatttcg acaacgatta caagactatg tatccatcct ttatggagtc cacatggtgg    480

gctttcaagc aacttcatga aaaaggtcaa gtttaccgtg gattcaaagt tatgccttat    540


587

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ttgattaaaa ccttgtataa gaagcctaag aatgaaaaat ataagattgt ggaaaaaatt   840

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tcctttaaat ttttggacgg tcaaattgcc ttgttgaaaa agatgtctaa catcgacttc  2040

caatatgatg attctgtgaa aagtgataat gtcatggaca gatggatttt agcttctatg  2100

caatctctag tacaattcat tcacgaagaa atgggtcagt acaaattata cactgtcgtt  2160
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588

ccaaaacttt tgaatttcat tgatgaattg acaaactggt atattagatt taatcgtcgt 2220

cgtttgaagg gtgaaaacgg tgttgaggac tgtttgaaag cattaaattc tttattcgat 2280

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aagtgtggtt tggaagccac cgacgatgtt ttagtggagt acgaattagt taaagatact 3060

atcgactttg aagccattgt caaagaacat tttgatatgt taagcaagac ctgtagatcc 3120

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aatgacacca ttttcaaatt aaaagtgttc aaattatga 3219

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<211>      324
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<213>      Saccharomyces cerevisiae

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aatggaaccc ttgtacgaca atggtacatc aggtttagtc tttgccatac cagcatttcc     180

ttcacacaac ttcaaaaaat tttcagccgt tttaggcact atgtcattgt acaactcaaa     240

aactatacgg ccttgggggtt tacctccaat agaaatatca aaaaagttt taggtctagt     300

589

cattttttact ccttgatcgc ctga

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<211>      363
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      472

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tctgatatca gagctcactt ggcccaatac tactctttcc aagccgctca tccaactgaa    180

acctacccag ttgaaatcgc tgaagccgtt ttcaactacg gtgacttcac caccatgttg    240

actggtattg ccccagacca agtgaccaga atgatcaccg gtgttccatg gtactccagc    300

agattaaagc cagccatctc cagtgctcta tccaaggacg gtatctacac tatcgcaaac    360

tag                                                                  363


<210>      473
<211>      1917
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      473

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aatatcaatg tcggcgtcgg tgacgatagc ggtaatgtca gcgcggtaag tatcgacgat    180

ggacccccact tcagggatat cttccactat ggacacgagg aaaattacaa acttgcgagc    240

agcggtatca ctaacctgaa ttcttcatcc cacgcccacc aaactttgtc tcccatttcc    300

attagtaatg catccactcc ggaaagtttt cccgagcacc ctttgggcct agaacgggaa    360

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taccttttaa gctccattaa ggcgaccaaa cgattaaaag atgctagacc gtttctgaag    480

ccggttgatc ctattgcttt gaacatcccg cattatttca actacgttca aaccccaatg    540

gatttgtctt taattgaaac aaaattgcag ggcaacgtgt atcattcagt agagcaagtc    600

acatcggact tcaaaacaat ggtggataat tgtttaaact ttaatggtcc agaatcttca    660
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ccaagagttt tacccgcttc tgccttgaag aaaacaagca gaaaccggaa aaaaaatgag    780

gatatggatt ccccacttgt cattagacgt tcagttagta ccaccaatga caatattggg    840

gaaagcggaa atagagaagg cgtcagtggt ggtagaccca aaagaacaat tcatccaccc    900

aaatcaaaag atttgtttga tatatatgaa aactccaaac caaaatcaaa gactttacaa    960

aaaaaattca ggacttgtct gaaaatacta aaggttttga tgagtaaaaa aaattcggat   1020

ataaattttc ccttttttaca acctgttgat ccgattgctt tgaatctacc aaattacttt   1080

gatgtcgtga agaatcctat ggatttgggt acaatatcaa ataatttaat gaactggaag   1140

tacaaaacaa ttgatcaatt tgtcgacgac ctcaaccttg tcttttataa ttgtttccaa   1200

ttcaatccag aaggcaatga agtccattca atgggcaaaa aactaaaaga gcttttcaat   1260

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gaggataact attcttcttc atattcatct gatgatgaat atgatgatga agacataaat   1380

gaaaacgata taactaatcc ggctattcaa tatttggaac aaaaactgaa gaaaatggag   1440

gttgaattgc aacaattgaa aagacaagag ttaagtaaat tatcgaagga aaggaagagg   1500

aagcatctag gtaaaacgct tttgcgtagg aaggcaatga agcattcagt tgacgattta   1560

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cgtatcatta aaaattcatt acccgcagat gaaatactaa cttccaatga agatgaaatt   1680

gaaattgatt tggatatttt agatgaagcg actattgcaa gaatttatga gagatatttt   1740

gagaaaaaaa ataacaacaa tagcaaaaga aaactaagtg gcaactactc gactgcgcca   1800

actaacaaga aaaagaaaac cttgaaattt ttggaaaagg atgaaatcat aaataataat   1860

aattattccg attctgaaga agacagtagt gatagtagcg acagtgacag tgattaa      1917


<210>      474
<211>      1152
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      474

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591

cagaggagtg aagtatttca agaatgtgtg aacctttca taaaaagaga tatcaaggat 180

tgcctagaaa aaatgtctga ggttggattt attgatatta ccgtttttcaa gtccaaccct 240

atgatattag atttatttgt cagcgcctgt gatattatgc ccagctttac caaattaggt 300

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tgctgtatca aggttattca gtttaactta actgatcaca ccgaacaaga agaaaaaact 480

ctggagcttg aatccataat gagtgatttc attttcgtat acataacgaa aatgaggaca 540

actatagatg tagttggctt acaagaatta atcgagatat tcatctttca ggtgaaggta 600

aaactgcatc ataaaaaacc ctcaccgaat atgtattggg cgctttgcaa aacattacct 660

aagttatctc aaccctaaa gggcctttac ttatctaaag atgtttccat agaggatgct 720

attctgaact caatagataa taaaatacaa aaagataagg cgaagtctaa aggtaaacaa 780

agaggagtga aacagaaaat acaccatttt cacgagccta tgttacacaa tagtagtgaa 840

gaacaggtta aggttgagga tgcgtttaat caacgcacct ctactgatag tagactccag 900

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acaggtctgc tgctactctt atgtttgaaa aaatataagt cattgatggc aatttttcaaa 1080

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<211>    2106
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<213>    Saccharomyces cerevisiae

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gaagtagcat tatcagaggt gatagcacaa gatattattg aagtagggggc tagtgttgag 180

gggcttgaac aattaagggc aaaatatggt gatctgcaaa tcttgaataa attggaaaag 240

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cagttagatg agttagctga acaaccgccg gatcaattca ctctagatga cgtaaaggcg 360

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cagtatgctg cttataacaa acttaaatca aaggttaccg gcaaatataa tgacgttatt 480

atacagaggt tagctactaa ctggagtaat acgtttgatc agaaattgtt agaagcgcaa 540

tgggatacgc aaaaatttgc atccacatca gttggtttgg ttaaatgtct gagagaaaat 600

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ggagatagcg aacgcccact ttcacgctca aacaataacc aagaacctgt gctatggaat 720

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tttaaatctt taagcagcat tttgagctta ccgtcacatg ctaccaatta taaatgtatg 1920

593

agtttacacg aactagtaaa aatattaaag ctaaagtatg atccaaacaa tcagcagttt 1980

ttaaacccag aatacattaa aacaggtaat ttcacatcat tgaaagaagc ttattccatt 2040

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<210> 476
<211> 1692
<212> DNA
<213> Saccharomyces cerevisiae

<400> 476

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gacattgcta ccgccccagc tgaaattgac agatgtatca gaaccactta cgtcacccaa 480

agaccagtct acttaggttt gccagctaac ttggtcgact tgaacgtccc agctaagttg 540

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595

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596

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597

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598

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602

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<212>      DNA
<213>      Saccharomyces cerevisiae

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gaaggtgagg gcaacgacga agatgacgac gacggcgacg gcgacgatat ggacgaggaa   360

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<213>    Saccharomyces cerevisiae

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aatgggaaca cttttggagg atccagttca atgggttctt ttggtggtaa taccaataat  360

gcatttaata taacagtaa cagtaccaat tccccgtttg gtttcaataa accgaataca  420

ggagggacct tgtttggttc gcagaataat aatagtgcag gtacttctag tttatttggc  480

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ggcagttcct tcggatcaaa accagttggt tcagggtcgc tgtttggcca gagcaacaac  780

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608

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609

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<212>    DNA
<213>    Saccharomyces cerevisiae

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cactgtttcg aactgttgaa cttgacctcc agatcgtttg ctgctgtgat cagagagctg    180

catccagaat tgagaaactg tgttactctc ttttatttga ttttaagggc tttggatacc    240

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tgtgtcgaga ttttttgacta ttacttacgt gatatcaaat ctaaattggc tgtgcaagat   1080

ccaaatttct taaaattgaa cattcaaatc tccaagatcg aacagtttat ggaagaaatg   1140


610

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aaagaaagat ccagatacga tgatgaattg gttccaaccc aacaagaaga agagtacaag 1260

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<212>    DNA
<213>    Saccharomyces cerevisiae

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611

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cacctggtag aagggaaatc taacagcaag gatgacctta gaatagaagc agacgcatca   1620

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<211>      2145
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      488

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                            612
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gcaaaaaccg cacaaaatga aaacaagtgt caacttaaac ttatatatag gaacactcct  1560

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tcgagtgatg taaatggtga cgtttccgag gaaagtgaaa atgaagttga cattgacgtt  1920

agcgatgact atgattcaga atatctgagt gaggagaata cattgacaag aaaaggtgaa  1980

gataggacag ataaatcttt tgggaaaaga gaattacaca atggcgctaa agattgtgat  2040

aggaattgtg atgatataga gatcttctca gaacccgtta ggcaactaca agataattct  2100

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<213>    Saccharomyces cerevisiae

<400>    489

613

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gaacattgta cgatactaag atcggatggc cagtacatga atctaagtgg agaacaggtg   240

tgcaaggtct gggcccggta cgccaagtac caagcccgac acgtagttat tcatgacgag   300

ttaagtgtgg cgtgtggaaa agtgcagctc agagccccca gcaccagtat tagaggtcat   360

aatgggctgc gaagcctgct aaaatgcagt ggaggccgtg taccctttgc caaattggct   420

attggaatcg gcagagaacc tgggtcccgt tctagagacc ctgcgagcgt gtcccggtgg   480

gttctgggag ctctaactcc gcaggaacta caaaccttgc ttacacagag tgaacctgct   540

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tcaaacttcg gaggtgctcc tcaaggtgga cacaacaacc atcaccgtca gacaataaca   360

acaataacgg tggatttggc ggtccaggcg gccctggcgg tcaaggtttc ggaagacaag   420

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614

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aacatgatta ctggtacttc tcaagctgac tgtgctatct tgattattgc tggtggtgtc   360

ggtgaattcg aagccggtat ctctaaggat ggtcaaacca gagaacacgc tttgttggct   420

ttcaccttgg gtgttagaca attgattgtt gctgtcaaca gatgggactc cgtcaaatgg   480

gacgaatcca gattccaaga aattgtcaag gaaacctcca ctttatcaa gaaggttggt   540

tacaacccaa agactgttcc attcgtccca atctctggtt ggaacggtga caacatgatt   600


615

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gtcaagggta agactttgtt ggaagccatt gacgccattg aacaaccatc tagaccaact    720

gacaagccat tgagattgcc attgcaagat gtttacaaga ttggtggtat tggtactgtg    780

ccagtcggta gagttgaaac cggtgtcatc aagccaggta tggttgttac ttttgcccca    840

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gaaccatact tattcaatga acctttgaag tcgatagtac gtgatattat ccaattgaga   2100

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617

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<212> DNA
<213> Saccharomyces cerevisiae

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catccacaaa tagaccaggc actaacaaaa catcgtacgt tgaatgagtc gcgtttattg 240

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618

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acttcgttgg catcattaaa ggctatccga tcaggaaatg aagaggaaag cgggaacgag  180


620

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621

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<213>      Saccharomyces cerevisiae

<400>      497

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gtcagtaaaa agaaaccagg gaataaggtc tctgatggaa gagataatgc acataattat  180

cacggggaag gccgcagaaa aagtagcaaa caacagaggt caagaacgcc ctataaggag  240

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ggtaatttca aattacgagg caggaaaact caagtttcca ttaatcattt gttgaatttc  360

cagttacctg aagtcgaaag ggaaaaaagt aggtcctctt caagtaagaa atcgaatagg  420

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atagcactat tgtttgcatt actcatcgct cgctgcacat gccacacaaa aaacacccac  180

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<213> Saccharomyces cerevisiae

<400> 499

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624

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625

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<211>      1809
<212>      DNA
<213>      Saccharomyces cerevisiae



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628

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<213>      Saccharomyces cerevisiae

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631

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gcagatagtt ctagtaaagg cagctcttca gccaagacaa ccacgtcctt aggcaaaagc   180

tcagtaacca gtaaggatgt ttcgtcaagt cataatgtca cttcaagcac taaaatgccc   240

aaaatcacca cgagcgctag tacaagctta tacaccaact ctagtttatg gagcaacaac   300

agtgtaatat caacttcatc tattacacct tccagcgttt atatcccggt tacggacgga   360

aataaattct tatatcaggc tcatcatcct aacggtactg tgttcattgc atttgctggc   420

tgtttaggtg caattctact atcactgacg ggtgcatgga ttgcattgaa tataaagtca   480

tggcgaagtg ctagaaagga aaataagctg agaaatctag aaaatcaata ccaacacgat   540

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641

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agatcatcta tgtttatttc acccaccgaa attctgcaat ctgatgccaa caactctaat    780

acatggtctc aaagcaatga gagtgctata tatgattcct tgtccagtac tccaagggaa    840

cctggtgcta cccaaatact gggaaagttt acagacagca ctaatccatt caattataca    900

tcatacaatt taagtcccga ctctgaagac cgctctactc caaaatcaaa tgttagtcag    960

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<210>       513
<211>       1356
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       513

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gcccatcctt acggttcatt gcaagggtct gataagtttg aagtgcgtgt gaaaagtaaa    180

caatttaaag atggggagtg gctgtaccat ataagtccta aaagtggctt cattcctgtt    240

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gatgatgcct accattctca ggaggatagc gttaccgaac atcgtggcaa cagaagattg    420

agttttcatt cgcacagaat tgaagaagtt cccaaaacag ggctgggctc ctcggcaggt    480

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ccttcgggat taactttatg gatgggcgat attaagaatg gttcagaaac agtaaaactg    840

gtccagaagg taaaaaattg gtatgattcg catatgccag aaagcttgaa aatatataca    900
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gaactcgatc atgcaaattc tagatttatg gatggactat ctaaactaga tcgcttacac  960

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tatgacgcca ttgcagtgat tactaagcaa gatgttgatc ttagggctca aaccgctaat 1260

gacaaaagat tttctaaggt tcaatggctg gatgtaactc aggctgactg gggtgttagg 1320

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<210>     514
<211>     1686
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     514

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aagtcacgtc atgggaagcc actacctgag cccgttgtcg acacccctcc ttattacatt  180

tctttgttaa catatctaaa ttatttgatt ctgattatat taggtcatgt tcacgacttc  240

ttaggtatga ccttccaaaa aaacaaacat ctggatcttt tagagcatga tgggttagca  300

ccttggtttt caaatttcga gagtttttat gtcaggagaa ttaaaatgag aattgatgat  360

tgcttttcta gaccaactac tggtgttcct ggtagattta ttcgttgtat tgatagaatt  420

tctcataata taaatgagta ttttacctac tcaggcgcag tgtatccatg catgaactta  480

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gttttttcga tgggttatgg tacaaatgca aacttgttca cgctttcct cgataaaaag  720

tgtttagtta tctctgacga attgaaccac acctctatta gaacaggtgt taggctttct  780

ggtgctgctg tgcgaacttt caagcatggt gatatggtgg gtttagaaaa gcttatcaga  840

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atgggtactt tcactaagtc gtttggtgct gctggtggtt acattgctgc tgatcaatgg 1140

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cctgttttag ctcaaactat ttcctcatta caaaccatta gtggtgaaat atgtcccgga 1260

caaggtactg aaagattgca acgtatagcc tttaattccc gttatctacg tttagctttg 1320

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aaattgaatt tgaaatcaaa ttccggcaaa tccagttacg acggtaaacg tcaaagatgg 1620

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aattga                                                                1686


<210>      515
<211>      1989
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      515

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atcagtatcc caagagattt ctcatcatca cctacatatt ctcctaagaa tacagtactt 180

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catttcagat ccctgggggtt gaatattcct gtcattctct gcaaaaataa atgtgattcc 360

atatcgaatg ttaatgccaa tgcaatggtc gtgtcagaga acagtgatga tgatatcgat 420

accaaagtgg aggatgaaga atttatccca atattaatgg agtttaaaga aatcgacact 480

tgcattaaga caagtgccaa gacacagttt gatcttaacc aagcgtttta tctttgccaa 540


644

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agggctataa cacacccaat atcaccttta tttgatgcca tggtaggtga actaaagcca  600

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ttagatgaca acgaaatctt gggcttacaa aaaaagtgct tcaataagag tatcgatgta  720

aacgaactga attttattaa agatttgctt ttggatattt ccaagcacga tcaagagtac  780

attaaccgca agctatacgt accgggaaaa ggcatcacca aagatggttt ccttgtactg  840

aacaaaatat acgctgaaag ggggagacac gaaactacat gggctatcct aagaactttc  900

cattacacag attccttgtg tattaatgac aaaattctcc atccgaggtt ggttgtccct  960

gacacttcca gtgtggaatt gagccccaag ggctacagat ttcttgtaga tatttttttg 1020

aagtttgata tcgacaatga tggtggtttg aataatcaag aattacatcg tctatttaag 1080

tgcacaccag ggctgcctaa actatggacc tcaacgaatt tcccccttctc cactgtcgta 1140

aacaacaagg gttgcatcac cttacaaggc tggctagcac aatggagtat gacgactttc 1200

ttgaactata gcacaactac cgcttacttg gtgtattttg gctttcagga agatgcaaga 1260

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tccaatatca atgacagaaa agtgttcaat tgctttgtca ttggaaagcc atgttgcggc 1380

aaaagctctt tgctagaggc cttcttgggc agatctttct cggaggagta ttctccgaca 1440

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attttgcaag aacttggaga acaggaatac gccatactag agaataagga taagttaaaa 1560

gaatgtgacg taatctgtct aacatacgat tccagcgacc cagaatcatt ctcctactta 1620

gtttcgcttc tagacaaatt cacacattta caagatctac cgttggtatt tgtagcttct 1680

aaggcagatt tggataagca gcaacaaagg tgtcaaatcc aaccagatga actggcagac 1740

gagctatttg tgaaccaccc actgcacata tcatccagat ggctaagttc ccttaatgaa 1800

ttgtttatta aaatcacaga agctgctctt gatcctggca aaaacactcc gggattgcca 1860

gaagaaacag cagcaaaaga tgtcgactac agacaaacgg ctctcatttt tgggtccact 1920

gttggattcg tagcactatg ttcctttacg ttaatgaaat tattcaaatc atcaaaattc 1980

tcaaaataa                                                        1989
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<210>      516
<211>      2004
<212>      DNA

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acggaagtgc ggtcattcta cgaagacgaa aagtctggtc taatcaaagt ggtaaaattc   180

agaactggtg caatggatag gaaaaggtct tttgaaaaaa ttgtcgtttc cgtcatggtc   240

gggaaaaatg tacaaaagtt cctgacgttt gttgaagacg aaccagattt ccagggcgga   300

ccaatccctt caaagtatct tattcccaag aaaatcaact tgatggtcta cacgttgttt   360

caagtgcata ctttgaaatt caatagaaag gattacgata ccctttctct tttttacctc   420

aacagaggat actataatga gttgagtttc cgtgtcctgg aacgttgtta cgaaatagcg   480

agtgccaggc cgaacgacag ctctacgatg cgtactttca ctgactttgt ttctggcaca   540

cctattgtaa ggagtcttca gaaaagcacc ataaggaaat atggatacaa tttggcaccc   600

tacatgttct tgttactaca cgtagatgag ctatcgattt tttctgcata ccaagcaagt   660

ttacctggcg aaaagaaagt cgacacagag cggctgaagc gtgatctatg cccacgtaaa   720

cccactgaga taaagtactt ttcacagata tgtaacgata tgatgaacaa aaaggaccga   780

ttgggtgatg ttttagctac agcgcaacgt atacgtcgac gatacaacaa gaacggttca   840

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646

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gctgcgttgc agcgtattgg gcttacggga ctggccaaga agtcgatgga catcaacgag 1680

ctcaaacggt cggaagatct cagcagaggt ctatccagct atccaacacg gatgtttaat 1740

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gaatcacagc ccgaagaagc actgaagctt cttttagccc tctttgaaat tgaaccagag 1860

tcgaaggcca ttgtagttgc aagcacaacc aacgaagtgg aagaattggc ctgctcttgg 1920

agaaagtatt ttagggtggt atggatacac gggaagcttg ggtgctgcag aaaaggtgtc 1980

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<210>      517
<211>      1152
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      517

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catgatacct taggtgccga tgaaggtaat gctttactcg atcaaatttt ggctgacacg 180

aatctatatc caccttggat gtgtgttctt ttatatgcat tttgttccgc tatggtcact 240

ccgtatgcct ttggtggcga ttgggtaaac ctggcaatct cattttttat ggggctttgt 300

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cacatctgct ttggtgcagt tacacaaggc tcattggcat taatcctgcc aggttatatt 480

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cacatctcac aactgccagt tatggtcttc atttcttgca ccggttatgt cgtaacatat 780

tgggccggta agcattttgc gaattcgaca gagtttactg ccgccttagc tgcatttgtc 840
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647

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gggttgcaaa gtgcaaatac aattgttaat gctaatgaaa ccattacgac aagcacctcc 1020

gatccatcgt cctcaatgtc atttggtatg acaatgattc aagtttgtgt cggtatttct 1080

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ttcagtttat aa                                                  1152


<210>      518
<211>      2424
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      518

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aatagccata tggggagagg tatatggaat ccatcgtacg taaatcaagg ctctcaaagg  180

tctccacagc agcagcatca gaatcatcac cagcagcagc agcagcagca acaacaacaa  240

caacagaatt ctcaattttg ctttgttaac ccttggaatg aggaaaaagt aactaattct  300

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gcgtacagac gacgtaaatc tagtctcgtt gtacctccag ccagggcacc tgccccaaat  420

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gttagaaata taggaattat agcccatatc gatgcaggta aaactaccac aacagagagg   180

atgctttatt atgcaggaat ctcaaagcat attggagacg tcgacactgg cgatacgata   240

actgattttt tagagcagga gagatcccga ggtatcacaa ttcaaagcgc tgcgatttca   300

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ggtacttctc ttgagcagtg taatcgttgt agggaatcga tgatagagac tttgactgaa   780

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tccgcacagt ttttgaacgc ttcaataaga aaactgacta tgaagaatat gattgtacct   900

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aattatctcc cttcgcccat tgaagccgaa ctaccagaac taaatgataa aaccgttcca  1020

atgaaatatg accccaaagt tggatgttta gtaaacaaca acaaaaatct ttgcattgct  1080

cttgcattca agtgattac ggatccaatc aggggtaaac aaatattcat tagaatttat  1140

tcaggtacac taaacagtgg caataccgtt tataattcta ctactgggga aaaatttaaa  1200

ttgggtaaat tactgatacc ccatgcggga acatcacaac ctgtaaatat tttaactgcg  1260

ggccaaatcg gattgcttac tggctctaca gtcgaaaaca acatatctac tggagataca  1320

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aggactttaa gtaataaaaa atcgatggaa gaagctttaa acactttaat tactgaagat  1500

cccagtcttt caatttctca aaatgatgag actggccaaa cggttttaaa cggtatgggt  1560
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660

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661

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663

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<213>      Saccharomyces cerevisiae

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664

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665

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<213>      Saccharomyces cerevisiae

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<210>     532



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668

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<213>        Saccharomyces cerevisiae

<400>        534

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669

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gctttggctg ctttgcaaat cgaagaccca tctgctgatg aattgagaaa ggctgaagtt  1800

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<213>      Saccharomyces cerevisiae

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gagaaagcta ccacagagga gaaagatcaa gaccaagaac agcccgccct gaagtcaaac   180

gaggacaggt actatgagga cccggtactc gaggacccgc attctgcagt cgccaatgca   240

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acagccgtca ataatgttgc taataaagat actttgaaaa tcaaagacct caagcagatg   360

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679

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cttgatggac tgctctaa                                                 558


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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      540
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cctatactta ttcatgggtt tttggccttt gtcaggctgt attggtttga aaggtacttc    420

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ccatcttctc aggaattgaa caagctagcc cagacgaaaa gtttccagaa attgcttggc    960

ttgcggagag atgaaggtga ccatgactac tttgacggtg ctcctcacaa atatatggtc   1020

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ccgagtccta aaacctcagg ccaagtagtt gaaaatcata gaaacttggc caagtcggcg   1140

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680

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gacaaactgg aacaaattga tcgtttacaa gatatgaaag ctaagggtaa gttgttagcc 2580

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atagcaacaa agttttgggg gaagcattaa                                    2670
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<212>      DNA

<210> Saccharomyces cerevisiae

<400> 541

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gaccgtgaat tcgtgccttg ttcgagtttg gacgtgcgca gaatctaccc aaaaggccca   180

ttacttgttc tcccggaaaa gatctacctt tattcagagc ccacggtaaa agagctttta   240

ccctttgatg tggtcatcaa cgttgctgaa gaggcaaacg atttacgaat gcaggttcct   300

gctgtcgagt accatcacta ccgatgggaa catgattcgc agattgcgtt ggacttgcca   360

tcattgacta gcatcataca cgcagctacg actaagcgag agaagatact gatacattgc   420

caatgtgggc tgtcgagatc cgcaacgctg attattgcat atataatgaa atatcataac   480

ttgagtctga ggcactcata tgatctgttg aaatcaaggg cagacaagat aaacccttcc   540

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<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    542

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tcaggttatt tatcttcatc atttgcgtta tgccaagtca tatctgcgta ccactggggt   240

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gtatcattgt taatactggg attttcacac aatttctatc aggctttggt ggcaagaagt   360

ttaatgggat tgctaaatgg taacgtcggc gttattagaa ccattattgg tgaaatagca   420

actgaaagaa aacatcaggc tttagctttc agtactatgc ctttattatt tcaatttggt   480

gccgttgttg ggcctatgat cggtggggtt cttgtattta gagatggaac aatgaatgaa   540

gtgccactat ggtttccaca ttttgcaaaa agaataatta ggtcatatcc gtacgccttg   600
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ccaaacgtgg tagtgtgcat gtttttgatg tttggtttaa ctaatgcaac attgtttttg    660

gaagaaacac atcctgcttt taaaaataga agagattacg gtttagaggt cggtgatttt    720

attaagaaga atatatttgg tatacagccg aaaagaagac cctggcaaaa gcgcattcag    780

gatgattcgg aaaacattca ccaccgtaat gagaatgtga acagcaatcg aggacaagat    840

agtgaagagg atgaaaatag tcccctagtg aatactacca atgacgatga tactgaaagc    900

atacaatcga ttgatcctat tttaacaaga agacagtctg taggcctgat taggacatat    960

tctctgcatg aaccaacaga cgctgtgcat gccaatatag atacagctcc agacggttgt   1020

aaagaaagta gtatatttca tcacgttttt catacaaaag tattttaccc tatatcggtg   1080

aattttatta tggctttaca tttgattgta tacaacgaat ttttgcctgt tttttttagct   1140

tatgatttag ccgtagatcc agaaaatcca aagaagctgg cttcaaaatt tccgtggaaa   1200

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aatgacgtcg cctgggtcag ttggtggtcg ttaagtcttt tttgtatggt agctctttat   1680

caaagttata agatagcacc aattgatgat aacgaaaatg agcttcatgg acagggtagt   1740

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      543

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683

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accgctattt tagaaaggga gattatctac atccccgaag atgacactga cagtattgac    240

agcgttgaca gcctcaagtg tataaactac aagctgcaca atctcgcgg cgaccaagtg     300

ctggacgcct gtgtgcaatt gatagacaag cacctgggcg ccaagtatcg ccgggcctcg    360

cgcattatgt acggcaacag gaaaccatgg aaggcaaaca aactcgcaga gatgaaaagc    420

gccggccttg tgtatgtctg ttactgggac aacggcgtgc taggtgcatt tacttcattc    480

atgcttacag aggagacggg tctcgtcgaa ggtgacgctt tacacgaggt tagcgtgccc    540

gtgatatacc tttacgaagt acatgtagct agcgcgcacc gcgggcatgg aatcggtcgg    600

cggctactgg agcatgcact gtgcgatggc gtagctcgac acacccgccg catgtgcgac    660

aatttcttcg gtgtagcact caccgtattc agtgataaca ctcgggcccg gcgactatat    720

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<213>      Saccharomyces cerevisiae

<400>      544

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attgtggatg ctgatggccg tgtatggcag agaggaggcg gttgctacga gttcactcag    360

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gccgtagact acgtggccat gggcaaggac ttcatggtca tagtggacga gggcggccgc    600
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atagtgcacg catccggtcg cctgcccact gggttcgagc tcaaacaaca gcaaaaaaga    660

cacaatctag tggtactgtg catgtggacc tcgatccacc tgtggaatgc gcgcctcaat    720

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gaaggcaagt ctcactgtta caatgtatac tgctggggct ggggagagca tggcaactgc    900

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<213>      Saccharomyces cerevisiae

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atgtcaaagc tattttctac tgtcaattct gcaagacata gtgtaccact aggcggcatg    180

agagattatg tgcacattaa gaaactagag atgaatacag ttcttgggcc tgattcctgg    240

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gagattgcga tggtaaatat tccatatctt tcctccatac atgaatcgtc tgatattaag    960

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caaagagact ttgctactgg agcggtggta gcgtcgtgta ttggtttcgg cagcgacatg 2520

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686

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<212>        DNA
<213>        Saccharomyces cerevisiae

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atttcaagga acgggaatga cagcaatatt aacatccagc cttcttccgt gccgcagcag   180

cagcagcagc agcagcaata ctaccgtaat ggcatgaatg aggctccaat acaagcgcca   240

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tataattttg agtattccaa tccacatatg aatgagattc ccctcatgca gcataacttc   360

accaaaccat cactaagcaa taatcgcgat aatgttaatg gtaagaaagc ttcctcattt   420

acccagagct cattttccaa tttttttcaaa cataagcatc aatttgggaa gtcaaagaaa   480

aacactaagg ggacaggagg tggtggagat ggtgatgatg acgatgaggt tatcttggat   540

gattctgcaa actccgacct aacattcaat gacattcaga ccttcggtca aagggcggt   600

gacaaatatg gatatggtgg tgattccact cctatcattc aacattggt gactaaagac   660

cgcggcaata tgagtaatac tgagtatagg aagtacatta ctaatcaaag gaaaaccgca   720

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ccaatcagtc aatcgtcaat ttcctcaaag aataattcag cttattcaat accgaacgta  1320

687

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gaaaacaagg gaaaactgaa tgttttgcaa ttatccactc ctcaacaaaa cgagttaaag 1500

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<210>     547

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tctactagcg gtaagaagag aaacaagctt ataaatctt gtggctttttg cagaaggaga  180

aaacttcgtt gtgatcagca aaaacctatg tgttctacat gcatttctag aaacttaaca  240

acctgtcaat atgctgaaga attcaacaaa aacatcgaaa agaaagctac ctatggtccc  300

tatcctaacg ccgatttact taagaaagtt gaagaactag aaaacaaaat acgtattcta  360

gaagctgaaa aaaacactaa ttcgtctgcg agctccatgt acacttcgcc aaatttccct  420

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gtaataaatc catatgccga ccggtactac ctacaaagta aacattccgg aagatcaaca  540

ctatacggcc ccacttctat gagaacccaa attgcaaata gtaattgggg gttcattgaa  600

aaatataaac aattatgggc gaaggttaaa gtagaagaa ataaatggaa gcaaaacaac  660

caaaaaacga tgtgcaggga actaggcctt ttggatgagt cggattggca gccagatcca  720

ttaatcaaac agatatgtcg tttcctacca tcatataaca aagctttgtc tattttagat  780

gatttctttta atgatggagc atgcaatgag atcaacgtga ttcttgataa ggcaaaagtt  840

agaagagact ttttagatta tttcatgccc gaaaaagagg taaaggcgga aggtgacaga  900

tccatagttt atattttatc caatccaaag aaaaattatt acaaagctgc tgtgatacta  960

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tatgagggga agctgaaaag atatttaaaa cttacaaggc caatgttgtt aactctttat 1440
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cttggcaacg ttattgaatt cagaaagttg accgaggaaa catggctagc acaaatcaaa 2160

caagaactag atccgcagag cgataatcca tcatcagaag ctaaaattgt gagtgatagg 2220

cagcgggatc tcagccttgc agttccaacg cccacgccct caataattcc aatgttaccc 2280

tcgcctggtg aaactaagaa ccatgcaaag agtcaatcag agatcattca gatgctgaca 2340

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<210>      548
<211>      2376
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      548

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agctctagtg gtactacact aaaattaata gctcttaata tcaagtccat atcagatgaa  180

gatgtgggat atatccaaaa tgttgaaaga ctgtctttaa ggaaaaatca cttaacatcc  240

ttaccagcga gtttcaagag gttatcaagg ctgcaatatc tggatttgca taataacaat  300

tttaaagaaa tcccatatat tttgacacaa tgccctcaat tagagatctt ggatctgtcc  360
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690

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tccaatgaga ttgaagcatt gccagatgaa atatcatcgt tttggcaaga taatattcgt  420

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ttaaacaagc tgagcatctt ggatttagag gataataaaa tacccaaaga agagcttgac  540

caagtacaga gttatactcc atttcatacg ggcatcccca aagaagaata ttgggcaatt  600

gcgatatcac gatatctaaa agatcatcct aacctaccta ctccagaacc taaaatatct  660

agagcagcga aaagaatggg attcataaat acgaacttgt ctaatggagc aatgaatgaa  720

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gtctcatcta atcaaacctc tgcaacatct ttcagtggta cagtcaatgc agaatcagaa  840

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atcagaaaaa tcgcctcttt ctgtaaagag aaggccgtag cggttaatgt agtatcatta  1080

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gaagacgaat cgcatgatca ggcgttaatc aagctgtgcc tcactatcat cacaaatttt  1200

aaacaaatta taacattgtt gagaaaaaat tttgagattt ttttcaaaga agacgatcta  1260

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cattcttttt cgaggcacga gacatcgtcc agtagtatca caagcggtgg aggacccgca  1440

gcaagtacga ccagtacaca ttgtagcgga aacataaaat tactgccgaa aacaaggagc  1500

acaagaacac catctgcatc tgcattgctt tcaaatagta atattctgac gggtgatacc  1560

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ggacaccaaa atgcaataag caatggaagt tctcaaacga acatgaatga agtaaaaact  1680

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aaaaaagagt cacaggcgca tgaacctaaa cagcatccgg ttatgacttc ttcaataatt  1800

aacgcatcaa atagtaataa cgtctcgaat gttaatataa ccccaccacc gatgaatggt  1860

ggtggtgccg cgaacagtag tgctaatgta gtggagacaa atattgacat tcaactgtat  1920

caaacgttgt ccacagtagt taaaatggtg agcgttgtat ataaccagtt aacttcagag  1980
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691

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atatccaaga tagccattgc tagcaccatg ggaaagcaaa ttttgacgga ctcgctagca 2040

cctaaaattc gtgatttgac ggaaacatgt cgtcaagcga tggatttatc caaacaattg 2100

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ttggagaagc tgaaaacgtg ggagataatg aattcgttct taaaagtaat aatatcaatt 2220

ctggctaata ctaaaatcgt aatgagcgac gtgcctaatt tgaatgagct gagacctaac 2280

ctagccaact tggcgaagat taccaaggat gtcactgtga tattggactt gagttcatac 2340

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<210>       549
<211>       1197
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       549

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aaggttccag aattggatgc atccaaggat tttgacgaaa ttatttttgg taacgttctt  180

tctgccaatt tgggccaagc tccggccaga caagttgctt ggctgccgg tttgagtaat  240

catatcgttg caagcacagt taacaaggtc tgtgcatccg ctatgaaggc aatcattttg  300

ggtgctcaat ccatcaaatg tggtaatgct gatgttgtcg tagctggtgg ttgtgaatct  360

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gttcttgttg atggtgtcga aagagatggg ttgaacgatg cgtacgatgg tctagccatg  480

ggtgtacacg cagaaaagtg tgcccgtgat tgggatatta ctagagaaca caagacaat  540

tttgccatcg aatcctacca aaaatctcaa aaatctcaaa aggaaggtaa attcgacaat  600

gaaattgtac ctgttaccat taagggattt agaggtaagc ctgatactca agtcacgaag  660

gacgaggaac ctgctagatt acacgttgaa aaattgagat ctgcaaggac tgttttccaa  720

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aaaggttggg gtgaggccgc tcatcaacca gctgatttta catgggctcc atctcttgca  900

gttccaaagg ctttgaaaca tgctggcatc gaagacatca attctgttga ttactttgaa  960
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692

ttcaatgaag cctttttcggt tgtcggtttg gtgaacacta agattttgaa gctagaccca 1020

tctaaggtta atgtatatgg tggtgctgtt gctctaggtc acccattggg ttgttctggt 1080

gctagagtgg ttgttacact gctatccatc ttacagcaag aaggaggtaa gatcggtgtt 1140

gccgccattt gtaatggtgg tggtggtgct cctctattg tcattgaaaa gatatga  1197


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<211>      846
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      550
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tttttttcaca ccaaccccct ctctttgaat atttcaacaa ccacggaaaa tggtgtgaat  120

tttactctga aggcgaagca gggcgtgaca gaaggcccca tccaaactag cgtagaagga  180

cggttttatg acaggaagga gggagtgtcg ctatctcaga gttggtcgaa ccagaacagg  240

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tttttgactc cccaatccat caagaacgcc aaatttaatt tgagctacgc ccaaaaatcg  360

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ttgggccacc gcgggtttgt tggcggcact gacatcgcat atgacacagc tgcgggttta  480

tgtgcacgct atgctatgtc aatcgggtat cttgccagag aatattcgtt tattttgtct  540

actaacaaca ggcaatgcgc aactgcttca ttttttcaaa acgttaaccg ctatttgcaa  600

gtgggaacta aagccacttt acaatcgaag acaagttcta atatgaacat tgaatttgtt  660

accagatacg taccagattc tatttcgcaa gttaaggcaa aaattgcaga ttcaggcctg  720

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      551
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gcggaagaac gtgccagcgt tgctacacca ttaaaggaca ttatgattgg tgatgaggca     180

agtgaagttc gctcttatct gcaaatatct tatcctatgg aaacggtat tattaagaat      240

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aaaatgtgtg aggtaatgtt cgaaaaatac gattttggcg agtttatgt tgccatccaa      420

gctgttctag cattgtacgc acaaggtttg tcttcaggag tcgtcgtcga ttccggtgac     480

ggtgttactc atatagtccc agtttacgaa tctgtcgttt tgagccactt aacaagaaga     540

ttagatgttg cgggtagaga cgttactagg catttgattg atctgctttc tcgtcgtggt     600

tatgcattta acagaactgc agatttcgaa actgtgcgtc agataaagga aaaattatgt      660

tatgtttcat atgatttaga cctagataca aaattggcta gagaaacaac cgcccttgtg     720

gaatcgtatg agttaccaga tggcaggaca atcaaagtgg acaagagag atttgaagca      780

ccagaatgtt tgttccaacc tggtttggtt gacgttgaac aacctggcgt gggcgagctg     840

ttatttaata ctgtgcaatc ggctgatgtt gatatcagaa gttccctgta taaggccatt     900

gttctttcag gtggttcaag tatgtaccca gggctgcctt cgagattaga gaaagaattg     960

aaacaattat ggtttagtag agttttacac aatgaccctt caagacttga taaattcaaa    1020

gttagaattg aagatcctcc aaggagaaag catatggttt tcattggtgg tgccgtttta    1080

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gggccatctg caatgactaa atttggtcca agatag                              1176


<210>       552
<211>       1587
<212>       DNA
<213>       Saccharomyces cerevisiae

<400>       552

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cccaagggta tggacaagat gattaagaca ctcgtggag aaatcatcat ctctaatgat      180
```

694

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ggccacacca ttctaaaaca gatggccatt ctgcatccgg tggccagaat gctagtagag  240

gtttctgccg cgcaggactc ggaagccggt gatggtacca cttctgtggt gatcttgacc  300

ggagctctat tgggtgctgc tgagaggctg ttaaacaagg gcatccatcc aaccatcatt  360

gcggactcct ttcaaagtgc tgcgaagaga tctgtcgata ttctttttaga aatgtgccat  420

aaggtttcgt tgagcgatag agaacagctg gttcgtgctg catccacttc tttgagttcc  480

aagattgtgt ctcaatactc ttcgtttttg gcgcccttgg cagtggactc cgtattgaag  540

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ggtatctctg ttagacgatc tggtactacg aacacctatg aagaacacat cttacaaccc 1500

gtacttgtta gtacaagtgc aattacctta gcgtctgaat gtgttaaatc catcttacgt 1560

attgatgata ttgcattcag ccgttaa                                      1587


<210>    553
<211>    630
<212>    DNA
<213>    Saccharomyces cerevisiae



                            695
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acagactatg cactaaggcg aagtccaata aagacaatcc aaatttctaa agctgcacaa   180

tttatgctgt atgaggaaac ggctgaagaa agaaacatag ctgtccacag acataatgaa   240

atatacaata ataacaattc tgtgagcaat gagaataatc cttcccaagt aaaagaaaac   300

ctttcacccg ctaaaatttg cccttatgaa agagcatttt taagggaagg aggaagaatt   360

gcattgaagg acttaagtgt tgacgaattc aaaggttaca tacaggatcc tctcaccgat   420

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acgccgccaa gaaattcgaa gatatctatt ttcttcacta gtaaacacca aggacagaac   540

ccagagacaa agatatcccg ttctaccgat gacgtcagtg aaaaaaaagt agtgagaaaa   600

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<210>        554
<211>        1671
<212>        DNA
<213>        Saccharomyces cerevisiae

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aattatgaag ctgttacag tgccgcggat atccagtctg ctggactgtc tctgaaaaac    180

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tcttcctctt ccaaagaagg gtctagcact tcctatatgc cctcaacaac ttcttcattg   480

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aatcctgata atcctgaatt atctagtacc gtatctcata atcgagcctg a            1671

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accgaacact tcggtatgaa gctattaagc agaaaggatt ttgaagaagc aaaatttagc    180

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gtttttagcg cacacggtgt cttagaacta actcacaatt ggggtactga aaaaaaccca    300

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697

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<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     556

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attaatgaag aaaaaaaagcc agaaccgcta ccgcagggcg tctggcaatg gctgaagccg    240

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tatcagaacg tcaagcaccg tggtagatat tttgcacatg ttttctgtgg atggattttc    480

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gctgtactag cgtcccctcg ttatgctaaa aaactatcct cgagaaccgt gttattccag    600

actgtcccta agcaatactt aagtgaagaa gagttttcta agttgtttga tggtgtgaaa    660

agagtctgga tcgcaagagg ttccggttca attgaagcaa tggtcaaagc aagggacaat    720

698

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cctgacaaga aaagaccaca tcataaaatt aacaaggttg ctaaattctt ttttggtaaa  900

aaagttgaca ccatatccta cattaaggag gagttgccca agttaaacca aaaggtgaag  960

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699

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ctaacaacta tatcaagaaa gccggatggt gatggcatca aatcattcac aattgcggta   360

aacaacactt ctacctgtcc tgaatcactt gcaaatagat tgattgtggt gattgaaatg   420

gattcgttaa tagtcaaaga atactgtccc caattccagc caataaaata cgatcccata   480

ataatcaacc ttaagtacaa aaggaggttt ttggatgttt ttggaactgc tgcctccgat   540

cggaatccac aggagccctt ggaccctaag ctattggacg tttttacaaa tacagagcgt   600

gagctaacat cagccttatt taacgaagaa gtggaatcag acatacgtaa aaggaatcag   660

ttaacggctg ctgatgagat taattacatt tgttgtaatt caactttatt gaagaatttt   720

ttagacaact gcaatgttaa tgtaaccgat gaagtaaaat tggaaattaa cgtacatagg   780

ctaagcataa ctgcattcac caaggccgtc tacggcaaaa ataacgacct tttaagaaat   840
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<211>      771
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      558

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aaaaccgcta cttctttggg tcagtcccca gttgtcatca ccatttataa atcactgtta  180

aaatattgga gtctttacga gttcatacat tttatttacc tctatactcc tattgatgcc  240

tttctgaatt tcttaccatt tacctctta cttatgtcgt ttggaagtat ttgcttgaca  300

agagagctgg tatatgactt cattgccttt atggaatctc aaaacaagct taccggattc  360


701

cttaataaga taacagaacc gaattttaac agttatttac tgttttcttc aatttataac    420

atttggtttg cagatgacac caatgacaaa ttcttattcg gtaaattaac tcagattttta   480

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gacaaaaatc gctatcaaaa cggtgaccgt gaatctacaa agaatggagc tgcttatcag    660

aagtcttcac aacaatcatc gtctttcgaa caaaattttta ccagcactga gttcccgaat    720

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<213>      Saccharomyces cerevisiae

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ggttccttgc tgggactagg aactgatata ggcggaagca tcagaattcc tagtagttac    720

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702

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703

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<210>     561
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<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     561

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704

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aaaacggatg ccatgttcca gcaccaactg ctaccgacgc aactgcaacc gtttcctcca    180

agtcatacac cactgttact gttactcact gtgacaacaa tggctgtaac accaagactg    240

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<211>      3483
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      562

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gatattccag actctaaagg ctcgccttca tttgagtatg atagcaatag cgcggatgaa    840

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ctagatctta tcaaattgct tgatatttgg acctcttttg atgaaaggga aataaaaagg 2520

706

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gacacactta cacattctgg caacgatctg gccatgtctt ctatgattca aagagagatc 2640

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gatactttac cagacatttt ggaaaataga ggaaattata aagattttgg tgtagctttt 2940

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gagccgtccg atatatcctc ttgggtttta attgatttga tttcgggaga gctattgaat 3060

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707

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708

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709

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713

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714

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<212> DNA
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715

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<213>    Saccharomyces cerevisiae

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gtaaaaaata gcgaactacc tagtgtgctg gttaatgaaa tggtcggaac caaagtaact    720

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cccacaaaag aaaggaaaag gtacttcaat atgagtgaac acgaggaaca aaaagagttg      240

cgaaagaagt atgagaccat gcaaccgctt agtggagaag ttgtgaccaa agatggagag      300

gtggttaaag aatctaagaa ataa                                            324

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<213>      Saccharomyces cerevisiae

<400>      572

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caaatggaac atgatatggc cgaccaagaa gagcatgacc tgtcatcatt cgagcgtaag   300

aaacttccaa ccgattttga cccaagtttg tatgatattt ctttccaaca aattgatgcg   360

gaacagagcg tactgaatgg tatcaaagat gaaaatacat ctaccgtggt aaggtttttt   420

ggtgtcacta gtgaaggaca ctctgtactt tgtaatgtta cagggttcaa gaactatctt   480

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719

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      573

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ttaactgggt taagcagtgg tactactgtt acgtttgaag gcacaaccac atttcagtac  240

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tcgggacata ccattgatgg tcaaggagca aaatggtggg atggcttagg tgatagcggt  360

aaagtcaaac cgaagtttgt aaagttggcg ttgacgggaa catctaaggt caccggattg  420

aatattaaaa atgctccaca ccaagtcttc agcatcaata aatgttcaga tttaaccatc  480

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ggccatggta tttctgtagg ttctgttggt ggccgttctg ataatacagt caatggtttc  720

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gcgaagaggg ttaaaatttt ggtgaaaaac gctactaact ggcaatggtc tggggtgtca 1020
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720

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<212>    DNA
<213>    Saccharomyces cerevisiae

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aagggtcaac aatttgcatt atacgaatca gaagctcagt taagcgttgc aaaagaagaa   300

gcccaaaagg caaaagaatt tttggataaa agatcagtga gggagaataa actaaatgaa   360

aaaacaaccc ttttacgtga tattaggacc atccaagatg ctttatctag cgggtcaacg   420

ccgaaagagt tattggagat taaacaaagg tacggcattc aagatttttc acaagaaaca   480

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agtctcattg atcgtattca aacgcgatta tccgaattgt tgtcgaatga tctaaaatgt   600

gatcaatttt tgaaggatca tggtgttgag gatcctttga ccttgaaaaa aaacatcaaa   660

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<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    575

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ccgcagtata aagaattgga agaactatac aaaaaatatc aagataaggg gtttgttatt   180

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ggaagtaatg ctgactctgt ctataattat ttgaaaagcc aaaaagcagg tttactaggt 360

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caaagatttt cctccttaac aaaaccatcg tccttggacc aagaaatcca aagcctgtta 480

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<211> 1473
<212> DNA
<213> Saccharomyces cerevisiae

<400> 576

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ttagcacagg aaattttttt tctggcggaa ttgaaatctc ctcttattac aaactatatt 240

gcaacaatgt tagaagatgt ctctatgtgg attgtcatgg aatattgcgg cggtggatca 300

tgttcagatt tactgaagcg aagttacgtc aacggtttgc ctgaagaaaa agtttccttc 360

attattcatg aagtcacctt gggtttgaaa tacctgcatg agcaaaggaa aattcatcgt 420

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caaactgtaa cgccgataac caacccaagt tcttcatcat ttagaaaatg tacgcaacca 1140


722

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<213>    Saccharomyces cerevisiae

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      578

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cagcagcgac aacaacagca gcagcagcaa cagcagcaac agcagtggat aaatcaacct  180

acggcggaaa attcggattt gaaggaaaaa atgaactgca gaatacgct caatgagtac  240

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gttgctccca cagcgccgcc ttccggcgat tttacaaatg tagggccaac ccagaatcgg  840

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725

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727

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728

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735

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736

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<210>      588
<211>      1860
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      588

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gatgaggtat ctggacaaac agcggagcct cgaaggacgg acagcaaatc catattacag     180

aggaaatgca aagaattctt cgactctttt aaaaggcagc tgccaccaga ccgtaattcc     240

gaactagagt cccaagaaaa aaacaacctg acaaagtcga tcaaatctcg tcacttagtc     300

atgatcagtc tcggtaccgg tataggtact ggtttactgg tcggtaatgg tcaggtgctg     360

ggaacagctg gtcctgccgg gttagtcctt ggttacggaa tagcatcgat catgctttac     420

tgtatcatcc aagcggcagg cgagttaggt ctctgttatg caggactaac cggcaattac     480

accagatatc cttctatttt agtcgaccct tcgttgggtt ttgcagtttc tgtggtttac     540

accattcaat ggctaactgt tctgccctta caattggtca ctgcggcaat gacagttaag     600

tactggacga gtgtaaatgc agacatcttt gttgccgtgg ttttcgtttt tgtaattatc     660

attaatctat ttgggtccag aggctatgct gaagccgagt tcattttcaa ttcctgtaag     720
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737

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aaaggtgtat gtacggtttt ctgttatgct gcattcagct acggtggaat tgaagttcta  900

cttctatctg ccgctgagca ggaaaaccca acaaaatcta ttcccaatgc ctgcaaaaaa  960

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atcgacaaag ttgacgataa cgatgatctt aaagagtatg aaaattcaga atcgtcggaa 1800

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<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      589

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gaccgcatag acgaacaccg ttgcaaagaa gtccagttat cttcattacg aagtctattg  180

tatgctatga ttttaaatag aaccataggc agcgagaccg gcgttttttc ttttctgctc  240
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738

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ttacttaaca ttacatattt attggattag                                     330


<210>    590
<211>    330
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    590

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ctcaagtctc cagtcattgg tactcgtacc aacatattcc tgcttgtggt atatagcagt    120

ttagttagtt ctttagtcgg tatgcgttcc tttcctttat atccgtcagg attaacttca    180

aggacttcac acagtttttc tatcttacta atattctttt tcgtcaccgt gtttatagtt    240

ctgatgggaa tatacctgcg aatcccagat attcgagcaa cagtagttgc aaacactttt    300

gtcctcaaca tgtcgagatt cattatctga                                     330


<210>    591
<211>    369
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    591

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ttcaaatctg gtttctcagt attacaaagt gctgcattgg atacagatga cgacctcgca    180

cgaggcttat cattgctaga cctgttacca ctcgtgctat tgtctccgtt tttcgaagag    240

gacgtagatg aagaggaggc tggcgacgta gaaggcctcg atggcttcgt atttgtcttc    300

cgtctactct tacctttata caaccaatct acgggcacat cgaactcggt gttagttatc    360

ataacctag                                                            369


<210>    592
<211>    366
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    592

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gaaactccag agtggcgtag gccggcttgt ttagttgcta gcatacttgt tcgagctctt   120

gagttctcct ggctttttctc cacgtgtctg cttgttgcct ttgatttcgc gagagactgc   180

ggactgccac cccactccgg gaaaacctgg agtgatggta aaggccctgc ggcgctttct   240

ttcggaaaaa ctaatacgaa agaagcaaca acaaattttt acaacaggct ggacgagaaa   300

agtggggaag agcaagcaga aaaaagaaaa gagaatagtc gttcttggat aatttatttа   360

ttataa                                                              366
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<210>     593
<211>     357
<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     593

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gccgctactg cgttacccgc acttcgccgc ccgccagaca gctgcgagac tctcgtcccg   120

ctactgtgta tcttttggtt cgtcttcgtt agtatgagcc cgctcccgcc ggctcgtgcc   180

aacaaatcag acaacaaagg cttaatctca gcagatcgta acaacaaggc tactctactg   240

cttacaatac cccgttgtac atccaagtcg tatacaaatg atttatcccc actcaaaatg   300

acattgctat ccgccggcaa gcacccaagg cctttccgcc aagagcaccg ttgctag      357
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<210>     594
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<212>     DNA
<213>     Saccharomyces cerevisiae

<400>     594

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aaacacaata gtttttttaga taggagtgaa gagataagcc tgtgtatgca tattaaatgg   120

tattttttcct ctggctattt ccattggtca ttaatcactc aaaattatat aatattcttg   180

tttttgtttc cttttaagtt ttcaatgcac tcatgttctt ctcgtatttg gggtaaaccc   240

ctttataagt tcgaaaatcg tcataacccg ttcagttcct tgtttatgtc tcacatacct   300

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740

tcagtactat actgttcaac atcctga                                             387


<210>      595
<211>      1044
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      595

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gaaggtgatt tactattttc atgttcgaaa gatagctcgg ccagtgtttg gtattcgttg   120

aacggtgaaa gattaggtac tttggatggt cacaccggta ccatttggtc tatcgacgtc   180

gactgtttca ccaagtactg tgttacagga agtgctgatt acagtatcaa attatgggat   240

gtgtcaaacg ggcaatgtgt tgctacatgg aaatcgcctg tccccgttaa aagagttgaa   300

ttttccccat gcggtaacta ctttctagct atcttggaca acgtcatgaa aaatccaggt   360

tccattaaca tatacgaaat tgaaagagat tccgccactc acgaattaac aaaggtctcc   420

gaagagccaa tccataaaat tatcactcat gaaggtttag acgctgccac cgtggctgga   480

tggtcgacta agggcaaata catcattgca ggccataaag acggtaagat cagcaaatac   540

gatgtgtcca acaactacga atacgtggat tccatcgatt tgcacgaaaa gtccatcagt   600

gacatgcaat tttctcctga tttaacatac tttattacat catccagaga tactaactcg   660

ttcttggtcg atgtatcgac tctacaagtt cttaagaaat acgaaacaga ctgtcctcta   720

aacaccgccg taatcacccc attgaaggaa ttcattattc ttggtggtgg tcaagaggcc   780

aaggatgtca ccaccaccag tgccaacgaa ggtaagtttg aagctaggtt ctaccacaag   840

atcttcgaag aagaaatcgg cagagtacaa ggccattttg gtcccttgaa cacagttgcc   900

attagcccac agggcacaag ttatgcctcc ggtggtgaag atgggttcat acgtctacac   960

catttcgaaa aatcttactt tgatttcaaa tacgacgtgg agaaggccgc cgaagctaaa  1020

gagcacatgc aagaagctaa ttaa                                          1044


<210>      596
<211>      447
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      596

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tcacctttcc aaaatgatgg ctacatcaaa gtaatggaac tcgtatcaca cattgtcatt   120

gaaataaatc attcacctac cgcaacaacg gatgaaacga gaaagcagaa taatccggag   180

ctgaaagtga aagaaccagt ttgtaacctc aagaagtggg aaaataacac taactttata   240

ttggaagatc atacgaagaa taaaacaaaa ctttctagca cagataggat acgtaagtgg   300

tttagaagac atatattaaa ggaagagatc gaaatccttt cccatggaaa acaattgagt   360

agtattgatg aggattattg cccttcaaat gttcttgtag gatgttcaag agatctaaat   420

aaactcagat catttcaaaa tttttag                                       447


<210>        597
<211>        1539
<212>        DNA
<213>        Saccharomyces cerevisiae

<400>        597

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gaggttgata aacagttgga atcaagcgga ttctcctctg attcctctct gatattgaat   120

aaaccagaag ttcgtcaata ctggtcatcc gtttcatctc atatttcacg ctcaggtgat   180

gtgtttacaa atgataaaga aaaaatttca tcctctattg gtgaggatgc gatggatatc   240

gacgcttcgc cctcattgat tgaaaaatat aactcttttc ccacaagaaa gattcttcct   300

gagcaggacg agtttgagaa cgacgttgag gacgatgctt cttcctcact gaaggaaaaa   360

tcacaaggtt cttgtgaaat tgaaattgct tctgaaattt catccgaaat tttaaatggc   420

acatcggcag acggtaattc cgagtttcac gacttcgctg agccccctcc ctctcagaat   480

gaatctgtcg ctctgtcttt tagtcaatcg aatgatttgg actttttgaa taatccaagc   540

ggatcaggct cttcaaacga tatcaataga agtacaagtt ccatttcact tcctagacat   600

gtgtcactag attttaacgt ttacaatagt ctttgcctca caaatgaggt gactgcatca   660

gaatcacata atgtggccaa atttcacctt ggcaagaaaa acaagaagag cttgctacca   720

agatggaaaa ccattgaaat gtacggggag gtagttaaga aaactcaaga catatattct   780

aattttcagt atgcacaata cattttaagg gtagggttgg ataccgaaaa actacacgaa   840

cttgttaagg aactggagga tgaaagcaat agcttctctg tagattcttt aaaggaatat   900


                                     742

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acctcccatg aagctgtggc agccaaaaag ttgatttaa                         1539


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<211>    1029
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    598

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ttccaagcta ccattgcgcc acttggtgca actttggtag acctgaaggt aaacggccaa  120

tcagtcgttc aaggttattc aaacgtacaa gactatttaa cagatggtaa catgatgggc  180

gctacagttg gtcgttatgc caaccgtatc gccaagggtg ttttcagcct ggatgatggt  240

cctcacaagt taactgttaa caattgtggt aacacaaatc acagcagtat cagttcctta  300

aatcttaagc agtacaaggc gtcccctgtt gagaatcctt ccaagggcgt ttacgttgtt  360

gaatttaaat tgttggatga tcacacacag cccaaccccta acgagtttcc aggtgacttg  420

gaagtcacag tgaagtacac tttgaatgtt gcagaaatga ctttagacat ggaataccaa  480

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aaatcgcttg aagttacaga gggggcattg cttccaactg gtaagatcat tgaaaggaac  660

attgctactt ttgattcaac taagcccacc gttttgcatg aagatactcc ggtctttgat  720

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tgcactttca ttattgacgc taacaaggat ttgaagacta cagattctgt gagtgtcaac   780

aaattggttc ctgtttttaa ggcctatcat cccgaatctc acatcaaatt tgaggtttcg   840

acgacagaac caaccgttca tttgtacacc ggtgataatt tatgtggcaa atttgtgcca   900

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agaggttgtg ttcttctgaa gcgcggcgag gtatacactt caaagactca gtacaaattc 1020

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<210>      599
<211>      4308
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      599

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aaaagggcca agcaacaaag taatagagca aaagtgacat ccacagcaag ctggacaggt   180

aaattgcctc atacaatctt acacgaaaca tgtcagaaac gaaaatggaa taaggtagag   240

tatgatatga agaaaatcgg tgataaaggt ttcattgcaa ttgcagtttt gtcattcact   300

gacccaaaga caaaagaaac attgactgca gaatgaacg atccaaccta tgacaaagct   360

tcaggaaaag gccttgtaat tcctcaagaa actccaattg aagctagaca catggcctcc   420

actattgcgc tatatcgcat tgcatacaac accaacctgc acatgatgct tccgccaaac   480

catagaaaaa catggtatgc cctcgacgat tttcgaaaag ataacctgaa aacagacgaa   540

aagcgtataa acaaactatt tgatcttgat cccttcaaga caatggtgga agacagaaag   600

ctcaaagccc aacgtgaaaa agaacaagtg gcccagaata tcaagcaca gaaagaacaa   660

gttgcacgaa ccattttatc tagccatggt ggaatttctt cttctggaaa ggacaggcaa   720

gagagaaaag tagcatctca taaaaactca cataatcctt cattagtgcg gtttccaaaa   780

aaggtttggg aaaattctat atttgttgac cttgatgaat cgtctagaca actgatagaa   840

acttcattga agagaaaat tgattggcaa gctaaaaaaa ttagccataa aaatgagaca   900

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cacgtagagg aagccatgct ttataaagat ccattgtctt tcttattgtt taacttaccg 1020
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744

gaagatgatt taccaccatt ttttcataaa aagaaaggtg atacaaaaaa caaggttgaa 1080

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tcttcagatg aagccttatt ggctttacaa caaaacgata tgaatgaaaa tgaagcggcc 1200

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agagaacaac tgcctgcctg gaagaagcaa aaggttatta tagatatcat caataaaaac 1860

gaagttgtat tgattactgg tgaaacaggt tcgggtaaat ccactcaggt cgttcagttt 1920

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746

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749

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aaagtcgcag caatctcaaa tgatgagcat tatgttgtaa gcaatgagag tctggaggag  600

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751
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tcagatgacg tcattgagct agctggtgga atgccaaacg agagattttt tcctatcgaa   180

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752

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<213>    Saccharomyces cerevisiae

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753

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gtaaatgtat atatacagct tgtgatttcg cgcgccgaat gggctgaaaa gcacagtata    180

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<213>      Saccharomyces cerevisiae

<400>      606

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754

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catttctcgt tccatgatgt gaatctgtca cttgatgatc tcaacattcc aaacgtgcaa  180

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759

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764

tctattatta acattcaact catcaaaatc aagacaaacc aaacatttga accgcagata 780

ttaaaatacg tatctgttct gaaattaatt gaacacatac ttatcatcat cgaaagtctg 840

atacatgtac ttattagatt tgtatcgaag cataaactaa tatgcatcaa ccggaaaaag 900

gcgtactgtc gagtatacct cgaaagagaa ttgagtttga agaaaaccta cttaaagaac 960

ttttacagtg taataagcgg tgtcccagaa aaagagttag ggggtctatt gaaaatactc 1020

aagatagtta ttctatcatt gctcgagaca tttgaaagca ttgaatggca gcacttaaaa 1080

cctttcctgg aaaaatttcc ggctcatgaa atatcgcttc agaagaaaag gaaatatata 1140

caggcggcct tattaattac tgccgaaaga aatttgatag cgcgctttcg attgtcaaga 1200

tggttcaatg agacagaaaa catttaa 1227


<210>      616
<211>      1956
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      616

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gaactaaaga aacaagaaaa agctgcaaag agagctgcaa tgaagcaggc taatggtata 180

tccattgaac aacagcaaca acaagcacaa atgaaaaaag agaagaaaca actacaacgt 240

gagcaacaac agaaaagaga gcaaaagcaa aaaaatgcca ataaaaaaaa acaaaatgaa 300

cgaaacgtga aaagagcac acttttttggt catctggaaa ctactgaaga aagaagagcg 360

acaattttag ctttaaccag tgcagtatca tctccaaaaa cttcgcgaat caccgctgct 420

gggttgatgg tccccgtggt ggctagtgca ttatcaggat ctaacgtatt aacggcttct 480

tccttgatgc ccgtgggtcc aaacgcgtcg tctactgtat ctgcatcagc tccagcttca 540

acaacaacga ctcttcctgc ctcttctgca gcactctctg ccggtaccag ttctgcgtca 600

acaaatactc aacagctat acaacaagag attgcttcat caaacgcttc tgatgttgcc 660

aagacattgg catctatctc gttagaggct ggtgagttta atgtcattcc cggtatatcg 720

tcagtgatcc ctaccgtgtt agaacaatca tttgacaact ccagcttgat atcgtctgtt 780

aaggaacttt tattgaataa agaccttatc catccgtcga tattattatt aacttctcat 840

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ctagcacact ataaaatcgt gggatccatc ccacgttgca tagccatgct agaggttttc  900

caaattgtta tcaaagacta tcaaacacct aagggaacta ccttgtcacg taacttaaca  960

agttatttgt cacaccagat tgatcttttg aaaaaagcta gacctttaag tgttactatg 1020

ggtaatgcta tcagatggtt aaagcaagaa atttcattaa ttgacccatc tacccccgac 1080

aaagccgcca aaaagacct ttgtgagaaa attgggcagt ttgctaaaga aaaaatcgaa 1140

ctggctgatc aactaattat agacaatgcc tctacacaaa ttgaagaatc tactactatt 1200

gtgacatatg gttcatcaaa ggttctaact gaactgttac tgcataatgc aatcagttta 1260

aagaaaaaca tcaaagtgat tgtcgtcgat tcgagaccac tatttgaagg gcggaaaatg 1320

gcagaaactt taagaaatgc tggtgtcaat gttatgtatg cacttattac aagtttggat 1380

acgatattca atatggatgt ggactatgtg tttttaggag cccattctat cctatctaat 1440

gggttcctat attcaagagc tgggacagca atgttggcta tgagcgctaa gagaagaaat 1500

atacctgtat tagtctgctg cgaaagtttg aagttttcac aaagagtaca attggatagt 1560

gtcacattta atgaactggc agatccaaat gacctggtta atatagatta cgaaaatcca 1620

gtcgagagac gcggtaataa aggtgcgtta ttaaaccaat ttatcaaaga aagaaaattt 1680

gaaaagaaaa agctagcaat ggagaataag ccaaagggta ataaaattgg cggtaagaaa 1740

ggatctgaag gagaaagcaa ggacgccagt aatgaagaag acagcaacag caaaaatatt 1800

ttggatggtt ggcaagagtt accttcgtta aatattgtca acatcttata cgatttaaca 1860

ccaccagaat atattaaaaa agtgatcact gaattcggcg ctttgccacc ttcatctgtc 1920

cctgttattt taagagagta caaaggttcc gcataa                           1956
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<210>    617
<211>    342
<212>    DNA
<213>    Saccharomyces cerevisiae

<400>    617

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atggtattga ggcgacataa gttgttagca cagcaaagat ggttgcgggt taagttttct   60

gatcgttctg ggagagtatt tacgttaaaa aataggaatc aattaagcat aatcatgccg  120

ttttgtgtgc tacatatctg tttcccacta tataaagtca cgttagaatg caatttatct  180

aatttactac cccattttag cgtcagtgga ttggtaaatc cctttgctag caaggtactg  240
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766

tcagaatatt tctccttcct ttcaaataat tgcaccaata tcttgccaat acttcacttg    300

agattgttct acaatatccg ctgtcttgga aagcaatttt ga    342


<210>      618
<211>      363
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      618

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tttgaaattg gttacttaga atatttctac tacatttcga taacaaatat aactattttg    120

aatttaaaag ttgagtatcc aaaaatttta gaaatacata caattacttc ccaattactt    180

cccaaatatt ctcccccctg gtttgatatc ataaaagcac cttatggcaa caagattccc    240

gggatagtaa tgctatttaa atgtatatct atttctcgaa tacttgtatc tttactccac    300

taccccttatg caagaagata cgcgatagtt tttgttcctt cctcttccta ctctgttaat    360

taa    363


<210>      619
<211>      462
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      619

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acaccacacc cacacccaca cccacaccca cacacaccca cacacacaca cccacacaca    120

cccacaccca caccacaccc acacccacac acaccacacc cacacaccac acccacaccc    180

acaccacacc acacccacac accacacacc accctatcta acctgtctct taacctaccc    240

tcacattacc ctacctcccc actcgttacc ctgccccact caaccatacc actcccaacc    300

accatccatc tctctactta ctactaccat ccaccgccca tcataaccgt taccctccaa    360

ttacccatat ccaactccac taccattacc ctgctattac cctaccatcc accatgtcct    420

actcactgta ctgttgttct accctccata ttgaaacgtt aa    462


<210>      620
<211>      1764
<212>      DNA

767

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atggacaagt atttgaattc atttgttgac caccttttcag agtggtcatc tcgtgccttt    60

aggaacaatt catcaagcgc taaccaaagt gcgtcgaaca aggaattaga acaagttttt   120

gaacagatca atgctatagt tgaaaaccac aataacaaat taaccactgc ctttgataag   180

atatcatatc gcgttgctca caagattaca cacttggtgg aaagccattc tttagtattc   240

aactacgcca ctttagttct catcgcaagt gctttggtcg ttattggctc atttacgtct   300

atttcttcta ttccatttac agctctacct cctacgagag aacactcatt gtttgatcct   360

acagattttg atgtggacca cgactgtcat gttatctacc gcgagaatga cgaagataaa   420

aagaaaaaga agaaaagcaa gaggtttttc gatatgatgg atgaaaaaca tgcgattata   480

ctgcccttaa ctagtggctg tactttactc gctctctatt ttgtgatcaa gaaactacac   540

ctaaactggc taaaatatgt ggtgaaaatt ttgaatttta atataacact gctaaatatc   600

ccagctggca catttgtcta ctcctacttt ctcaactcac ttttcagaaa cctatcacat   660

ttagcttctt ggaatcccct ggttgtttta ccaaggtatc gtgtaacaat agctgatgat   720

aacgaagacc tgaacaagat aggcgggttt gttaccaatt tgaattacaa agatggattg   780

accaactcag ttgttcacaa gaaaacattg gatgagattg aaaaagatca ttggatgaag   840

cattttaca gaagagaatt agttgaaccg aaggatatta aatcgaagag gcagatcagc   900

aacatgtatt tgaatagcgc attaattgtt tcgttcgttc tgtccatcgt ttctaccgta   960

tatttctatt tatcacccaa tgattggtta atatccaatg ctgtcagtat gaatatggct  1020

atttggtcca ttgctcaatt aaaattgaag aatttaaaat caggggccct aatcctaatt  1080

gctctatttt tttacgacat ttgctttgtc tttggtaccg atgtaatggt tacagtagct  1140

actaaccttg atattcccgt aaaactaagc ttaccagtca gtttaatac agctcaaaac  1200

aacttcaatt tttcaatact tggtctgggt gatattgcct tgcctggtat gtttattgcg  1260

atgtgctaca aatatgacat ctggaagtgg caccttgatc atgatgacac tgaattccac  1320

ttttttgaact ggtcatacgt tggaaaatat tttattactg ctatggttag ttacgttgct  1380

tctttggtat ctgccatggt ctccttgtcc attttcaata ctgctcaacc ggctttatta  1440

tacattgttc cttccttgtt gattagtact attttggtag cttgctggaa caaggatttt  1500
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768

aagcagtttt ggaattttca gtatgatacg attgaagtgg ataaaagttt aaaaaaagcg 1560

atagaaaaaa aggagaactc tataacttat tcgaccttca tcctatcaga atactataat 1620

gatgccgaca agtatgcctt gcttggtgat gatgtaaacg aaaattttga cgatgatgaa 1680

gaattcgtgc aagaggaaga tctcagtgac agctctgagg aagagctttc tgaagaagat 1740

ctcttggatg acgaatcttc ttga                                    1764


<210>      621
<211>      1929
<212>      DNA
<213>      Saccharomyces cerevisiae

<400>      621

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ttagacacct ccggcaactc accagccaat gaacacacag ctaccacaat tacacagaat  180

cacagcgtgg tggcctcaaa cggagacgtc gcattcatcc aggaactgc taccgaaggc  240

aatacagaga ttgtaactga agaagtgatt gagaccgatg ataacatgtt caagacccat  300

gtgaagactt taagctccaa agagaaggca cggtataggc aagggtcctc taactttata  360

tcgtatttcg atgatatgtc atttgaacac aggcccagta tattagatgg gtcagttaac  420

gagcccttca gaccaaatt cgtgggacct actttagaaa aggagatcag aagaagggag  480

aaagagctaa tggccatgcg caaaaattta caccaccgca gtcctcccc agatgctgtc  540

gactcagtag ggaaaaatga tggcgccgcc ccaactactg ttccaactgc cgccacctca  600

gaaacggtgg tcaccgttga aaccaccata atttcatcca atttctccgg gttgtacgtg  660

gcgttttgga tggctattgc atttggtgct gtcaaggctt aatagacta ttattaccag  720

cataatggta gcttcaagga ttcggagatc ttgaaattta tgactacgaa tttgttcact  780

gtggcatccg tagatctttt gatgtatttg agcacttatt ttgtcgttgg aatacaatac  840

ttatgcaagt ggggggtctt gaaatggggc actaccggct ggatcttcac ctcaatttac  900

gagtttttgt ttgttatctt ctacatgtat ttaacagaaa acatcctaaa actacactgg  960

ctgtccaaga tcttcctttt tttgcattct ttagttttat tgatgaaaat gcattctttc 1020

gccttctaca atggctatct atggggtata aaggaagaac tacaatttc caaaagcgct 1080

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cttgccaaat acaaggattc tataaatgat ccaaaagtta ttggtgctct tgagaaaagc 1140

tgtgagtttt gtagttttga attgagctct cagtctttaa gcgaccaaac tcaaaaattc 1200

cccaacaata tcagtgcaaa aagctttttt tggttcacca tgtttccaac cctaatttac 1260

caaattgaat atccaagaac taaggaaatc agatggagct acgtattaga aaagatctgc 1320

gccatcttcg gtaccatttt cttaatgatg atagatgctc aaatcttgat gtatcctgta 1380

gcaatgagag cattggctgt gcgcaattct gaatggactg gtatattgga tagattattg 1440

aaatgggttg gattgctcgt tgatatcgtc ccagggttta tcgtgatgta catcttggac 1500

ttctatttga tttgggatgc cattttgaac tgtgtggctg aattgacaag atttggcgac 1560

agatatttct acggtgactg gtggaattgt gttagttggg cagacttcag tagaatttgg 1620

aacatcccag tgcataagtt tttgttaaga catgtttacc atagttcaat gagttcattc 1680

aaattgaaca agagtcaagc aactttgatg accttttttct taagttccgt cgttcatgaa 1740

ttagcaatgt acgttatctt caagaaattg aggtttttact tgttcttctt ccaaatgctg 1800

caaatgccat tagtagcttt aacaaatact aaattcatga ggaacagaac cataatcgga 1860

aatgttattt tctggctcgg tatctgcatg ggaccaagtg tcatgtgtac gttgtacttg 1920

acattctaa                                                       1929


<210>      622
<211>      358
<212>      PRT
<213>      Glycine max

<400>      622

Met Thr Met Leu Gln Lys Met Ala Glu Leu Met Glu Tyr Ser Tyr Leu
1               5                   10                  15

Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Met Arg Leu Val Tyr
            20                  25                  30

Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr Ala Tyr Gln Arg Thr Trp
        35                  40                  45

Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met Val Asn His
    50                  55                  60

Gly Gly Ile Thr Phe Ile Ser Glu Gln Val Ser His His Pro Pro Met
65                  70                  75                  80

Ser Ala Gly His Ala Glu Thr Glu His Phe Thr Tyr Asp Val Thr Ser
```

770

Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Val Asp Val Tyr Pro Val
            100                     105                     110

Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val Leu Asp Leu
            115                     120                     125

Val Pro Pro Pro Thr Lys Val Ser Asn Leu Ile Phe Gly Arg Thr Trp
        130                     135                     140

Ile Asp Ser Pro Gly Glu Met Ile Leu Thr Asn Leu Thr Thr Gly Asp
145                     150                     155                     160

Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly Tyr Glu Val
                165                     170                     175

Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu Pro Lys Ile Leu Met Thr
            180                     185                     190

Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln Val Cys Asp Ser Glu Gly
            195                     200                     205

Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu Ile Trp Arg Val Ala Asp
        210                     215                     220

Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr His Phe Ala His Lys Ile
225                     230                     235                     240

Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu Leu Ala Ser Asp Ser Arg
                245                     250                     255

Leu Arg Pro Asp Arg Met Ala Leu Glu Lys Gly Asp Leu Ser Thr Ser
            260                     265                     270

Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg Gln Arg Ala Glu Lys Arg
            275                     280                     285

Asn Arg Glu Ala Lys Gly His Lys Phe Thr Pro Arg Trp Phe Asp Leu
        290                     295                     300

Thr Asp Glu Val Thr Pro Thr Pro Trp Gly Asp Leu Glu Val Tyr Gln
305                     310                     315                     320

Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala Ala Val Asp Ser Ser Glu
                325                     330                     335

Cys Ile Glu Val Pro Asp Ile Arg Pro Glu Phe Asn Pro Trp Gln Tyr
            340                     345                     350

Asp Asn Leu Asp Ala Glu
        355

771

<210> 623
<211> 300
<212> PRT
<213> Glycine max

<400> 623

Met Cys Asn Asn Gly Gln Ser Pro Leu Asp Arg Phe Ile Ser Val Val
1               5                   10                  15

Ala Trp Cys Ile Ser Thr Thr Arg Pro Val Thr Phe Gly Val Ala Pro
            20                  25                  30

Tyr Asn Pro Ile Leu Gly Glu Thr His His Val Ser Arg Gly Asn Leu
        35                  40                  45

Asn Val Leu Leu Glu Gln Ile Ser His His Pro Pro Val Thr Ala Leu
    50                  55                  60

His Ala Thr Asp Glu Lys Glu Asn Ile Glu Met Leu Trp Cys Gln Arg
65                  70                  75                  80

Pro Asp Pro Lys Phe Asn Gly Thr Ser Val Glu Ala Lys Val His Gly
                85                  90                  95

Ile Arg Gln Leu Lys Leu Leu Asn His Gly Glu Thr Tyr Glu Met Asn
            100                 105                 110

Cys Pro Arg Leu Leu Leu Arg Ile Leu Pro Val Pro Gly Ala Asp Trp
            115                 120                 125

Ala Gly Thr Val Asn Ile Arg Cys Leu Glu Thr Gly Leu Val Ala Glu
    130                 135                 140

Leu Ser Tyr Arg Ser Ser Ser Phe Leu Gly Ile Gly Gly Asn His Arg
145                 150                 155                 160

Val Ile Lys Gly Lys Ile Leu Asp Ser Ser Ser Leu Lys Val Leu Tyr
            165                 170                 175

Glu Val Asp Gly His Trp Asp Arg Thr Val Lys Val Lys Asp Thr Asn
            180                 185                 190

Asn Gly Lys Val Arg Val Ile Tyr Asp Ala Lys Glu Val Met Ser Gly
            195                 200                 205

Leu Glu Thr Pro Ile Leu Lys Asp Ile Glu Gly Val Trp Gln Thr Glu
    210                 215                 220

Ser Ala His Val Trp Gly Glu Leu Asn Gln Ala Ile Val Ser Lys Asp
225                 230                 235                 240

Trp Glu Lys Ala Arg Glu Ala Lys Leu Lys Val Glu Glu Arg Gln Arg
                245                 250                 255

772

Glu Leu Val Arg Glu Arg Glu Ser Lys Gly Glu Thr Trp Ile Ser Lys
        260                 265                 270

His Phe Val Val Ser Asn Asn Lys Glu Gly Trp Gln Cys Ser Pro Ile
        275                 280                 285

His Lys Ser Val Pro Ala Ala Pro Ile Thr Ala Leu
    290                 295                 300


<210>       624
<211>       355
<212>       PRT
<213>       Glycine max

<400>       624

Met Ala Glu Leu Met Glu Tyr Ser Tyr Leu Leu Asp Met Ala Asp Lys
1               5                   10                  15

Thr Glu Asp Pro Tyr Met Arg Leu Val Tyr Ala Ser Ser Phe Phe Ile
            20                  25                  30

Ser Val Tyr Tyr Ala Tyr Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile
        35                  40                  45

Leu Gly Glu Thr Tyr Glu Met Val Asn His Gly Gly Ile Thr Phe Ile
    50                  55                  60

Ser Glu Gln Val Ser His His Pro Pro Met Ser Ala Gly His Ala Glu
65                  70                  75                  80

Thr Glu His Phe Thr Tyr Asp Val Thr Ser Lys Leu Lys Thr Lys Phe
            85                  90                  95

Leu Gly Asn Ser Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr
            100                 105                 110

Leu Lys Arg Asp Gly Val Val Leu Asp Leu Val Pro Pro Pro Thr Lys
        115                 120                 125

Val Ser Asn Leu Ile Phe Gly Arg Thr Trp Ile Asp Ser Pro Gly Glu
    130                 135                 140

Met Ile Leu Thr Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe
145                 150                 155                 160

Gln Pro Cys Gly Trp Phe Gly Ala Gly Arg Tyr Glu Val Asp Gly Tyr
            165                 170                 175

Val Tyr Asn Ser Ala Asp Glu Pro Lys Ile Leu Met Thr Gly Lys Trp
            180                 185                 190

773

Asn Glu Ala Met Asn Tyr Gln Val Cys Asp Ser Glu Gly Glu Pro Leu
        195                     200                 205

Pro Gly Thr Glu Leu Lys Glu Ile Trp Arg Val Ala Asp Thr Pro Lys
        210                     215                 220

Lys Asp Lys Phe Gln Tyr Thr His Phe Ala His Lys Ile Asn Ser Phe
225                     230                 235                 240

Asp Thr Ala Pro Lys Lys Leu Leu Ala Ser Asp Ser Arg Leu Arg Pro
                245                 250                 255

Asp Arg Met Ala Leu Glu Lys Gly Asp Leu Ser Thr Ser Gly Tyr Glu
        260                     265                 270

Lys Ser Ser Leu Glu Glu Arg Gln Arg Ala Glu Lys Arg Asn Arg Glu
        275                     280                 285

Ala Lys Gly His Lys Phe Thr Pro Arg Trp Phe Asp Leu Thr Asp Glu
        290                     295                 300

Val Thr Pro Thr Pro Trp Gly Asp Leu Glu Val Tyr Gln Tyr Asn Gly
305                     310                 315                 320

Lys Tyr Thr Gln His Cys Ala Ala Val Asp Ser Ser Glu Cys Ile Glu
                325                 330                 335

Val Pro Asp Ile Arg Pro Glu Phe Asn Pro Trp Gln Tyr Asp Asn Leu
                340                 345                 350

Asp Ala Glu
        355


<210>      625
<211>      414
<212>      PRT
<213>      Zea mays

<400>      625

Met Ala Thr Lys Glu Glu Ala Ser Ala Val Pro Ala Ala Ser Lys Thr
1                   5                   10                  15

Ser Trp Ser Ser Phe Leu Lys Ser Ile Ala Ser Phe Asn Gly Asp Leu
            20                  25                  30

Ser Ser Leu Thr Ala Pro Pro Phe Ile Leu Ser Thr Thr Ser Leu Thr
            35                  40                  45

Glu Tyr Ser Ala Tyr Trp Cys Glu His Pro Ala Leu Phe Val Ala Pro
        50                  55                  60

Ala Arg Glu Pro Asp Pro Ala Lys Arg Ala Leu Leu Val Leu Lys Trp

774

Phe Leu Ser Thr Leu His Gln Gln Tyr Cys Ser Arg Ser Glu Lys Leu
     85      90     95

Gly Ser Glu Lys Lys Pro Leu Asn Pro Phe Leu Gly Glu Leu Phe Leu
     100     105     110

Gly Lys Trp Ile Glu Asp Glu Asp Val Gly Glu Thr Arg Leu Ile Ser
     115     120     125

Glu Gln Val Ser His His Pro Pro Ala Thr Ala Tyr Ser Ile Val Asn
     130     135     140

Glu Lys His Gly Val Glu Leu Gln Gly Tyr Asn Ala Gln Lys Ala Ser
145     150     155     160

Phe Ser Ser Thr Ile Gln Val Lys Gln Leu Gly His Ala Tyr Leu Ser
     165     170     175

Leu Thr Pro Pro Gly Lys Asp Ala Asn Asn Glu Asp Asp Arg Glu His
     180     185     190

Tyr Leu Ile Thr Leu Pro Asn Leu His Ile Glu Ser Leu Ile Tyr Gly
     195     200     205

Thr Pro Phe Val Glu Leu Glu Lys Ser Cys Lys Ile Ala Ser Ser Thr
     210     215     220

Gly Tyr Ile Ser Lys Ile Asp Phe Ser Gly Lys Gly Trp Leu Ser Gly
225     230     235     240

Lys Lys Asn Thr Phe Ser Ala Val Leu Tyr Lys Glu Ser Asp Gly Glu
     245     250     255

Lys Asn Pro Leu Tyr Thr Ala Asp Gly Gln Trp Ser Ser Ser Phe Thr
     260     265     270

Ile Arg Asp Ala Arg Ala Lys Lys Asp Ile Glu Thr Phe Thr Ile Ser
     275     280     285

Asn Leu Lys Thr Thr Pro Leu Thr Val Ala Pro Leu Asp Glu Gln Asp
     290     295     300

Glu Trp Glu Thr Arg Arg Ala Trp Arg Asp Val Ala Ala Ala Ile Glu
305     310     315     320

Arg Gly Asp Met Glu Ala Thr Ser Asn Ala Lys Thr Lys Ile Glu Val
     325     330     335

Ala Gln Arg Glu Leu Arg Lys Lys Glu Lys Glu Gln Gly Glu Glu Trp
     340     345     350

Glu Arg Arg Phe Phe Lys Arg Val Asn Glu Lys Asp Glu Pro Thr Phe

775

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           355                  360                  365
Met Arg Leu Ala Ala Met Leu Asp Leu Thr Gln Gly Ile Glu Ser Asp
    370                 375                 380

Arg Thr Gly Gly Val Trp Arg Phe Asp Pro Ser Arg Ala Val Asp Ala
385                 390                 395                 400

Asn Pro Pro Tyr His Lys Val Gly Gly Glu Gly Leu Gly Leu
                405                 410


<210>      626
<211>      434
<212>      PRT
<213>      Saccharomyces cerevisiae

<400>      626

Met Ser Gln His Ala Ser Ser Ser Ser Trp Thr Ser Phe Leu Lys Ser
1               5                   10                  15

Ile Ser Ser Phe Asn Gly Asp Leu Ser Ser Leu Ser Ala Pro Pro Phe
            20                  25                  30

Ile Leu Ser Pro Thr Ser Leu Thr Glu Phe Ser Gln Tyr Trp Ala Glu
        35                  40                  45

His Pro Ala Leu Phe Leu Glu Pro Ser Leu Ile Asp Gly Glu Asn Tyr
    50                  55                  60

Lys Asp His Cys Pro Phe Asp Pro Asn Val Glu Ser Lys Glu Val Ala
65                  70                  75                  80

Gln Met Leu Ala Val Val Arg Trp Phe Ile Ser Thr Leu Arg Ser Gln
            85                  90                  95

Tyr Cys Ser Arg Ser Glu Ser Met Gly Ser Glu Lys Lys Pro Leu Asn
            100                 105                 110

Pro Phe Leu Gly Glu Val Phe Val Gly Lys Trp Lys Asn Asp Glu His
        115                 120                 125

Pro Glu Phe Gly Glu Thr Val Leu Leu Ser Glu Gln Val Ser His His
    130                 135                 140

Pro Pro Met Thr Ala Phe Ser Ile Phe Asn Glu Lys Asn Asp Val Ser
145                 150                 155                 160

Val Gln Gly Tyr Asn Gln Ile Lys Thr Gly Phe Thr Lys Thr Leu Thr
                165                 170                 175

Leu Thr Val Lys Pro Tyr Gly His Val Ile Leu Lys Ile Lys Asp Glu
            180                 185                 190
```

776

Thr Tyr Leu Ile Thr Thr Pro Pro Leu His Ile Glu Gly Ile Leu Val
        195             200             205

Ala Ser Pro Phe Val Glu Leu Gly Gly Arg Ser Phe Ile Gln Ser Ser
    210             215             220

Asn Gly Met Leu Cys Val Ile Glu Phe Ser Gly Arg Gly Tyr Phe Thr
225             230             235             240

Gly Lys Lys Asn Ser Phe Lys Ala Arg Ile Tyr Arg Ser Pro Gln Glu
                245             250             255

His Ser His Lys Glu Asn Ala Leu Tyr Leu Ile Ser Gly Gln Trp Ser
            260             265             270

Gly Val Ser Thr Ile Ile Lys Lys Asp Ser Gln Val Ser His Gln Phe
            275             280             285

Tyr Asp Ser Ser Glu Thr Pro Thr Glu His Leu Leu Val Lys Pro Ile
    290             295             300

Glu Glu Gln His Pro Leu Glu Ser Arg Arg Ala Trp Lys Asp Val Ala
305             310             315             320

Glu Ala Ile Arg Gln Gly Asn Ile Ser Met Ile Lys Lys Thr Lys Glu
            325             330             335

Glu Leu Glu Asn Lys Gln Arg Ala Leu Arg Glu Gln Glu Arg Val Lys
            340             345             350

Gly Val Glu Trp Gln Arg Arg Trp Phe Lys Gln Val Asp Tyr Met Asn
    355             360             365

Glu Asn Thr Ser Asn Asp Val Glu Lys Ala Ser Glu Asp Asp Ala Phe
    370             375             380

Arg Lys Leu Ala Ser Lys Leu Gln Leu Ser Val Lys Asn Val Pro Ser
385             390             395             400

Gly Thr Leu Ile Gly Gly Lys Asp Asp Lys Lys Asp Val Ser Thr Ala
            405             410             415

Leu His Trp Arg Phe Asp Lys Asn Leu Trp Met Arg Glu Asn Glu Ile
            420             425             430

Thr Ile